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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:17:16 ; Search time 22.3492 Seconds
(without alignments)
463.411 Million cell updates/sec

Title: US-09-939-226-5
Perfect score: 1841
Sequence: 1 MDYOVSSPIYDINITYTSEPC.....ERASSVYTRSTGEQISVGL 352

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgnt2_6/ptodaca/1/1aa/5A.COMB.pep.*
2: /cgnt2_6/ptodaca/1/1aa/5B.COMB.pep.*
3: /cgnt2_6/ptodaca/1/1aa/6A.COMB.pep.*
4: /cgnt2_6/ptodaca/1/1aa/6B.COMB.pep.*
5: /cgnt2_6/ptodaca/1/1aa/PCBUS.COMB.pep.*
6: /cgnt2_6/ptodaca/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1841	100.0	352	4	US-09-087-232A-13
2	1841	100.0	352	4	US-08-861-105-14
3	1841	100.0	352	4	US-08-575-967A-2
4	1841	100.0	352	4	US-08-833-752-5
5	1835	99.7	352	4	US-09-045-583-52
6	1835	99.7	352	4	US-09-534-185-52
7	1826	99.2	352	3	US-08-466-343D-2
8	1814	98.5	352	4	US-09-517-605-5
9	1546	84.0	354	4	US-08-724-984A-2
10	1364	74.1	347	1	US-08-461-244-3
11	1364	74.1	360	1	US-08-450-393A-4
12	1364	74.1	360	4	US-08-446-669-4
13	1364	74.1	360	4	US-09-045-583-50
14	1364	74.1	360	4	US-09-534-185-50
15	1364	74.1	360	5	PCT-US95-00476-4
16	1350	73.3	360	4	US-08-833-752-7
17	1345	73.1	360	4	US-09-045-583-51
18	1345	73.1	360	4	US-09-534-185-51
19	1324	66.5	344	3	US-08-466-343D-9
20	1324	66.5	374	1	US-08-450-393A-2
21	1324	66.5	374	4	US-08-446-669-2
22	1224	66.5	374	5	PCT-US95-00476-2
23	1055	57.3	355	1	US-08-012-988A-2
24	1055	57.3	355	1	US-08-450-393A-5
25	1055	57.3	355	4	US-08-446-669-5
26	1055	57.3	355	4	US-09-239-938-1
27	1055	57.3	355	5	PCT-US95-00476-5

28	1028	55.8	355	4	US-08-833-752-9	Sequence 9, Appl1
29	1009	54.8	355	4	US-09-045-583-53	Sequence 53, Appl1
30	1009	54.8	355	4	US-09-534-185-53	Sequence 53, Appl1
31	958	52.0	184	4	US-08-833-752-4	Sequence 4, Appl1
32	958	52.0	215	4	US-09-087-232A-17	Sequence 17, Appl1
33	958	52.0	215	4	US-08-833-752-6	Sequence 6, Appl1
34	938.5	51.0	355	4	US-08-575-967A-4	Sequence 4, Appl1
35	938.5	51.0	355	4	US-08-847-296B-1	Sequence 1, Appl1
36	938.5	51.0	355	4	US-09-045-583-54	Sequence 54, Appl1
37	938.5	51.0	355	4	US-09-534-185-54	Sequence 54, Appl1
38	919	49.9	360	4	US-08-875-573-20	Sequence 20, Appl1
39	919	49.9	360	4	US-09-232-878-2	Sequence 2, Appl1
40	919	49.9	360	4	US-09-045-583-55	Sequence 55, Appl1
41	919	49.9	360	4	US-09-534-185-55	Sequence 55, Appl1
42	899.5	48.9	355	4	US-08-833-752-8	Sequence 8, Appl1
43	885	48.1	360	4	US-08-833-752-10	Sequence 10, Appl1
44	746.5	40.5	355	1	US-08-461-244-2	Sequence 2, Appl1
45	746.5	40.5	355	4	US-09-045-583-56	Sequence 56, Appl1

ALIGNMENTS

RESULT 1
US-09-087-232A-13
Sequence 13, Application US/09087232A
Patent No. 6153431

GENERAL INFORMATION:

APPLICANT: Oullent et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS: ADDRESSSEE: Baker & Botts, L.L.P. attn. Lisa Koie

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/087,232A

FILING DATE: 28 MAY 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/048,057

FILING DATE: 30 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: KOIE, LISA B.

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: AP 31115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2628

TELEFAX: (212) 765-2519

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 100.0% Score 1841; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2, 7e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MDYOVSSPIYDINITYTSEPCIKIVKQIAKLLPLYSVIFGVCNMLVILLINCKR 60
Db 1 MDYOVSSPIYDINITYTSEPCIKIVKQIAKLLPLYSVIFGVCNMLVILLINCKR 60

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QY 61 LKSMIDYILNLAISDIFLLVPPMAHYAAQMPGNTMCOLLGLVFIGFSSGIFPII 120
DB 61 LKSMIDYILNLAISDIFLLVPPMAHYAAQMPGNTMCOLLGLVFIGFSSGIFPII 120
QY 121 LITIDRYLAVVAHVAFLKARVTFGVTSVITWVAVAFASLPGLIIFTRSQKEGLHYTCSS 180
DB 121 LITIDRYLAVVAHVAFLKARVTFGVTSVITWVAVAFASLPGLIIFTRSQKEGLHYTCSS 180
QY 181 HEPYQOYQPMKFOPLKIVILGLVPLVMVTCYSGILKTLRCNREKRRHRAVRLIFTI 240
DB 181 HEPYQOYQPMKFOPLKIVILGLVPLVMVTCYSGILKTLRCNREKRRHRAVRLIFTI 240
QY 241 MIVYFLFAPYINIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
DB 241 MIVYFLFAPYINIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
QY 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352
DB 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352

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RESULT 2

```

; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELMETER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: USES THEROF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14

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Query Match 100.0%; Score 1841; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2,7e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDYVSSPIYDINNTTSEPCQKINVKQIARLLPLYSIVTFEGVGNNLVLLINKR 60
DB 1 MDYVSSPIYDINNTTSEPCQKINVKQIARLLPLYSIVTFEGVGNNLVLLINKR 60
QY 61 LKSMIDYILNLAISDIFLLVPPMAHYAAQMPGNTMCOLLGLVFIGFSSGIFPII 120
DB 61 LKSMIDYILNLAISDIFLLVPPMAHYAAQMPGNTMCOLLGLVFIGFSSGIFPII 120
QY 121 LITIDRYLAVVAHVAFLKARVTFGVTSVITWVAVAFASLPGLIIFTRSQKEGLHYTCSS 180
DB 121 LITIDRYLAVVAHVAFLKARVTFGVTSVITWVAVAFASLPGLIIFTRSQKEGLHYTCSS 180
QY 181 HEPYQOYQPMKFOPLKIVILGLVPLVMVTCYSGILKTLRCNREKRRHRAVRLIFTI 240
DB 181 HEPYQOYQPMKFOPLKIVILGLVPLVMVTCYSGILKTLRCNREKRRHRAVRLIFTI 240
QY 241 MIVYFLFAPYINIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
DB 241 MIVYFLFAPYINIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
QY 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352
DB 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352

```

RESULT 3

```

; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

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NAME/KEY: misc.feature
OTHER INFORMATION: /- "88c amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 1841; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVSSPIYDINNTYSEPCOKINVKQIAARLLPPLSLVIFGVGMVLILLINCKR 60
DB 1 MDVSSPIYDINNTYSEPCOKINVKQIAARLLPPLSLVIFGVGMVLILLINCKR 60
QY 61 LKSTDIYLLNLAISDFELLTPFMAHYAAQMDFGNTMQLTGLYIFGFSGIFPII 120
DB 61 LKSTDIYLLNLAISDFELLTPFMAHYAAQMDFGNTMQLTGLYIFGFSGIFPII 120
QY 121 LITDRILAVHVAFAKARTVTEGVTSVTWVAAPASLPGIIFRSQEGHLYCSS 180
DB 121 LITDRILAVHVAFAKARTVTEGVTSVTWVAAPASLPGIIFRSQEGHLYCSS 180
QY 181 HFPYSOYQFMKNFTLKIIVILGLVPLLVNYICSGILKTLRCRNEKKRRRAVRLIFTI 240
DB 181 HFPYSOYQFMKNFTLKIIVILGLVPLLVNYICSGILKTLRCRNEKKRRRAVRLIFTI 240
QY 241 MIYFLFMAPYNIYLLNTFOEFGLNCCSSNNLDQAMOYETLGMTHCCINPIIYAFV 300
DB 241 MIYFLFMAPYNIYLLNTFOEFGLNCCSSNNLDQAMOYETLGMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFOKHAKRFCKCSIFQEAPEBASSVYTRSTGEQISVGL 352
DB 301 GEKFRNYLLVFFOKHAKRFCKCSIFQEAPEBASSVYTRSTGEQISVGL 352

RESULT 4

US-08-833-752-5
Sequence 5, Application US/08833752
Patent No. 6448375

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASGART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Altmann, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-833-752-5

Query Match 100.0%; Score 1841; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVSSPIYDINNTYSEPCOKINVKQIAARLLPPLSLVIFGVGMVLILLINCKR 60
DB 1 MDVSSPIYDINNTYSEPCOKINVKQIAARLLPPLSLVIFGVGMVLILLINCKR 60
QY 61 LKSTDIYLLNLAISDFELLTPFMAHYAAQMDFGNTMQLTGLYIFGFSGIFPII 120
DB 61 LKSTDIYLLNLAISDFELLTPFMAHYAAQMDFGNTMQLTGLYIFGFSGIFPII 120
QY 121 LITDRILAVHVAFAKARTVTEGVTSVTWVAAPASLPGIIFRSQEGHLYCSS 180
DB 121 LITDRILAVHVAFAKARTVTEGVTSVTWVAAPASLPGIIFRSQEGHLYCSS 180
QY 181 HFPYSOYQFMKNFTLKIIVILGLVPLLVNYICSGILKTLRCRNEKKRRRAVRLIFTI 240
DB 181 HFPYSOYQFMKNFTLKIIVILGLVPLLVNYICSGILKTLRCRNEKKRRRAVRLIFTI 240
QY 241 MIYFLFMAPYNIYLLNTFOEFGLNCCSSNNLDQAMOYETLGMTHCCINPIIYAFV 300
DB 241 MIYFLFMAPYNIYLLNTFOEFGLNCCSSNNLDQAMOYETLGMTHCCINPIIYAFV 300
QY 301 GEKFRNYLLVFFOKHAKRFCKCSIFQEAPEBASSVYTRSTGEQISVGL 352
DB 301 GEKFRNYLLVFFOKHAKRFCKCSIFQEAPEBASSVYTRSTGEQISVGL 352

RESULT 5

US-09-045-583-52
Sequence 52, Application US/09045583
Patent No. 6287805

GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Mandagouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: NMI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide

FRAGMENT TYPE: Internal
US-09-045-583-52

Query Match

99.7%; Score 1835; DB 4; Length 352;

Best Local Similarity 99.4%; Pred. No. 8.3e-144;
Matches 350; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCQKINVKQIARLLPPLYSVLFIFGFVGNMLVILLINCKR 60
Db 1 MDYVSSPIYDIDYITSEPCQKINVKQIARLLPPLYSVLFIFGFVGNMLVILLINCKR 60
QY 61 LKSMIDYLLNLTAISDLFFLLVPEFAHAAQMDGNTMCOULLGLYETIGFSSGIFETI 120
Db 61 LKSMIDYLLNLTAISDLFFLLVPEFAHAAQMDGNTMCOULLGLYETIGFSSGIFETI 120
QY 121 LITIDRYLAIVAAVFAKARVTFGVVTSVITWVAVFASLPGIITRSQKESLHTCSS 180
Db 121 LITIDRYLAIVAAVFAKARVTFGVVTSVITWVAVFASLPGIITRSQKESLHTCSS 180
QY 181 HPPYSQYQWKNFQTKIYILGLVPLVWVICSGLTKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPPYSQYQWKNFQTKIYILGLVPLVWVICSGLTKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLFMAPYNIIVLLNTFOEFEGNLNCSSNRDLQAMQVETLGMTHCCINPIIYAFV 300
Db 241 MIVYFLFMAPYNIIVLLNTFOEFEGNLNCSSNRDLQAMQVETLGMTHCCINPIIYAFV 300
QY 301 GEFERNYLLVFQKHIAKRFCKCSIFQOEAPERRASSVYTRSTGDEISVGL 352
Db 301 GEFERNYLLVFQKHIAKRFCKCSIFQOEAPERRASSVYTRSTGDEISVGL 352

RESULT 6
US-09-534-185-52
Sequence 52, Application US/09534185
Patent No. 6403767

GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses Thereof

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNT-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match 99.7%; Score 1835; DB 4; Length 352;
Best Local Similarity 99.4%; Pred. No. 8.3e-144;
Matches 350; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCQKINVKQIARLLPPLYSVLFIFGFVGNMLVILLINCKR 60
Db 1 MDYVSSPIYDIDYITSEPCQKINVKQIARLLPPLYSVLFIFGFVGNMLVILLINCKR 60
QY 61 LKSMIDYLLNLTAISDLFFLLVPEFAHAAQMDGNTMCOULLGLYETIGFSSGIFETI 120
Db 61 LKSMIDYLLNLTAISDLFFLLVPEFAHAAQMDGNTMCOULLGLYETIGFSSGIFETI 120
QY 121 LITIDRYLAIVAAVFAKARVTFGVVTSVITWVAVFASLPGIITRSQKESLHTCSS 180
Db 121 LITIDRYLAIVAAVFAKARVTFGVVTSVITWVAVFASLPGIITRSQKESLHTCSS 180
QY 181 HPPYSQYQWKNFQTKIYILGLVPLVWVICSGLTKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HPPYSQYQWKNFQTKIYILGLVPLVWVICSGLTKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLFMAPYNIIVLLNTFOEFEGNLNCSSNRDLQAMQVETLGMTHCCINPIIYAFV 300
Db 241 MIVYFLFMAPYNIIVLLNTFOEFEGNLNCSSNRDLQAMQVETLGMTHCCINPIIYAFV 300
QY 301 GEFERNYLLVFQKHIAKRFCKCSIFQOEAPERRASSVYTRSTGDEISVGL 352
Db 301 GEFERNYLLVFQKHIAKRFCKCSIFQOEAPERRASSVYTRSTGDEISVGL 352

RESULT 7
US-08-466-343D-2
Sequence 2, Application US/08466343D
Patent No. 6025154

GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFER, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 99.2%; Score 1826; DB 3; Length 352;
Best Local Similarity 98.9%; Pred. No. 4.6e-143;
Matches 348; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY	1	MDQVSSPIYDINNTYTSBPCOKINXKOIARLLPXTLSVTFEGFVGNMLVILILNCR	60
Db	1	MDQVSSPIYDINNTYTSBPCOKINXKOIARLLPXTLSVTFEGFVGNMLVILILNCR	60
QY	61	LKSMTDIYLLNLAISDLFEPLLTPVPWANHAAAQMDPGNMCOLLTLYIFGFSGIFETI	120
Db	61	LESMDIYLLNLAISDLFEPLLTPVPWANHAAAQMDPGNMCOLLTLYIFGFSGIFETI	120
QY	121	LTITDRYLAIVHAVALKARVTFGVTSVITWVAVAFSLPGIIFTRSQKEGLHYTCS	180
Db	121	LTITDRYLAIVHAVALKARVTFGVTSVITWVAVAFSLPGIIFTRSQKEGLHYTCS	180
QY	181	HPFYSQYQPMKNFOYLKVIILGLVPLVMVYCYSGILTLTLCRNREKRRHRAVRLIFTI	240
Db	181	HPFYSQYQPMKNFOYLKVIILGLVPLVMVYCYSGILTLTLCRNREKRRHRAVRLIFTI	240
QY	241	MIYVFLFAPARNIYLLMTPOEFEGFNSSNRDLQAQVETLGMTCCINPIIYAFV	3000
Db	241	MIYVFLFAPARNIYLLMTPOEFEGFNSSNRDLQAQVETLGMTCCINPIIYAFV	3000
QY	301	GEKFRNLYLVFQKHIARKFCSCSIFQOEADEBRASVYTRSTGEOEISVGL	352
Db	301	GEKFRNLYLVFQKHIARKFCSCSIFQOEADEBRASVYTRSTGEOEISVGL	352

RESULT 8
 US-09-517-605-5
 : Sequence 5, Application US/09517605
 : Patent No. 6391567
 : GENERAL INFORMATION:
 : APPLICANT: Littman, Dan R.
 : APPLICANT: Kwon, Douglas S.
 : APPLICANT: van Kooyk, Yvette
 : APPLICANT: Gajtenbeck, Theo
 : TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
 : TITLE OF INVENTION: CELLS
 : FILE REFERENCE: 1049-1-017
 : CURRENT APPLICATION NUMBER: US/09/517,605
 : CURRENT FILING DATE: 2000-03-02
 : NUMBER OF SEQ ID NOS: 17
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 5
 : LENGTH: 352
 : TYPE: PRN
 : ORGANISM: Homo sapiens
 US-09-517-605-5

[illegible]

Db 301 GEFKNYLLVFFQKHIAKHECKCSIFQAEAPERASSVYTRSTGEQEIISGL 352

RESULT 9
US-08-724-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6389055

GENERAL INFORMATION:
APPLICANT: Derek Bergsma, Mary Bravner, and Usman Shabon
TITLE OF INVENTION: NO. 638805561 Mouse Genomic Clone of the CC-
TITLE OF INVENTION: CKR5 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
FILING DATE: October 3, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-724-984A-2

Query Match	84.0%: Score 1546; DB 4;	Length 354;
Best Local Similarity	81.4%: Pred. No.5.le-120;	
Matches 288;	Conservative 29; Mismatches 35; Indels 2; Gaps 1;	
QY 1 MDYOVSSP--TYDINYYTSEPCQKINWKOIARLLPPLSYLVTFEGFVGNMLVILIINC	58	
1 MDPFGSVPTIYDIDYDYGMSAPCQKINWKOIAQOLLPLXSLVTFIFGFGNNMVFILILSC	60	
QY 59 KRKLSMTDIYVLNLAISDLDFLLTVPEWAAHAAAQMDFGNTMCCOLLGLYVTFGFSGIFF	118	
61 KKLKSVTDIYLLNLAISDLLETLTLPFWAAHAAENEMIGINCKVETGVYHIGYRGIEF	120	
QY 119 IILITIDRYLAVNAVPAALKARATYTFEGVTSVIINWVAEVSLSGIIITTSQKESLHTC	178	
121 IILITIDRYLAVNAVPAALKATVTPNFGVITSVTWVVAVFAFSLPEIITPSQKEGFHYTC	180	
QY 179 SSHPEYSOYOPMKNEQFTKIYIIGLVPLVWVCYSGIILITLLRCRREKRHRVAVLIE	238	
181 SPHEPHQYHNKMSFQILKMWILSLIPLVLIITLCISGILITLLRCRREKRHRVAVLIE	240	
QY 239 TIMIVPELFMAVYNIVLLNTFOEFGFLNCCSSNRLDQAQOVETLGMTACQIPIYA	298	
241 AIMIVPELFEMTPYNIIVLLTTFGEFEGFLNCCSSNRLDQAQOAVETLGMTACQIPIYA	300	
QY 299 FVGEKFRNYLLVFQKHAKRFCCCSIFQOEAPEBASSVYTRSTGEDEISVGL	352	
301 FVGEKFRNSYLVSEFRKHIYKRFCKRCSIFQODNDRVASSVYTRSGEHEVSTGL	354	

Patent No. 6403767

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION: <Unknown>

PRIORITY INFORMATION:

APPLICATION NUMBER: 09/045,583

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragoras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNT-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)742-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-534-185-50

Query Match

Best Local Similarity 74.1%; Score 1364; DB 4; Length 360;

Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

10 VQINVTSPCKIVKQIAARLLPPLYSLVFIFGVGNMLVILLINCKRLKSMIDYIL 69

24 FDIYD-GAPCHKFVYKQIGALPLPLYSLVFIFGVGNMLVILLINCKRLKCLTDIYL 81

70 LNLAIISDLFLLVFPMAHYAAQMDPGNTMCOILLTGLYFGFSGIFFIILLTDIYLA 129

82 LNLAIISDLFLLVFPMAHYAAQMDPGNTMCOILLTGLYFGFSGIFFIILLTDIYLA 141

130 VYHVAVALKARTYTGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSSHPYSQYOF 189

142 IYHVAVALKARTYTGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSSHPYSQYOF 197

190 WKNFOTLKIVYIGLVPLLVWVYICSGILKTLRCKNEKKRRARAVLFTIMIVYFLFWA 249

198 WNNFHTIMRNIILGLVPLLVWVYICSGILKTLRCKNEKKRRARAVLFTIMIVYFLFWA 257

250 PYNIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAFVGEKRRYLL 309

258 PYNIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAFVGEKRRYLL 317

310 VFOKHIKRRFCCKCSIFQOEADEPARASVYTRSTGQDEISVGL 352

318 VFRKHITKRCCKCPVYRETVDGVTSTWPTSGQEVASGL 360

PCT-US95-00476-4

Sequence 4, Application PC/TUS9500476

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOTACTANT

TITLE OF INVENTION: PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner & Carson

STREET: 201 N. Figueroa Street, 5th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90012-2628

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/00476

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Berliner, Robert

REGISTRATION NUMBER: 20,121

REFERENCE/DOCKET NUMBER: 5555-291

TELECOMMUNICATION INFORMATION:

TELEPHONE: 310-977-1001

TELEFAX: 310-977-1003

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-00476-4

Query Match

Best Local Similarity 74.1%; Score 1364; DB 5; Length 360;

Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

10 VQINVTSPCKIVKQIAARLLPPLYSLVFIFGVGNMLVILLINCKRLKSMIDYIL 69

24 FDIYD-GAPCHKFVYKQIGALPLPLYSLVFIFGVGNMLVILLINCKRLKCLTDIYL 81

70 LNLAIISDLFLLVFPMAHYAAQMDPGNTMCOILLTGLYFGFSGIFFIILLTDIYLA 129

82 LNLAIISDLFLLVFPMAHYAAQMDPGNTMCOILLTGLYFGFSGIFFIILLTDIYLA 141

130 VYHVAVALKARTYTGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSSHPYSQYOF 189

142 IYHVAVALKARTYTGVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSSHPYSQYOF 197

190 WKNFOTLKIVYIGLVPLLVWVYICSGILKTLRCKNEKKRRARAVLFTIMIVYFLFWA 249

198 WNNFHTIMRNIILGLVPLLVWVYICSGILKTLRCKNEKKRRARAVLFTIMIVYFLFWA 257

250 PYNIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAFVGEKRRYLL 309

258 PYNIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAFVGEKRRYLL 317

310 VFOKHIKRRFCCKCSIFQOEADEPARASVYTRSTGQDEISVGL 352

318 VFRKHITKRCCKCPVYRETVDGVTSTWPTSGQEVASGL 360

Search completed: June 3, 2003, 15:23:37
Job time: 37.3492 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:09:10 ; Search time 64.5644 Seconds
(without alignments)
726.472 Million cell updates/sec

Title: US-09-939-226-5

Perfect score: 1841
Sequence: 1 MDQVSSPIVDINITYTSEPC.....ERASSVYTRSTGEQETISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1841	100.0	352	18	AAW27407 Human CCR5. Homo
2	1841	100.0	352	18	AAW27123 Human chemokine re
3	1841	100.0	352	19	AAW23835 Human CC chemokine
4	1841	100.0	352	20	AAW8232 HIV-1 co-receptor
5	1841	100.0	352	22	AAW80111 Human CCR5 protein
6	1841	100.0	352	22	AAW82948 Human HIV-1 co-rec
7	1841	100.0	352	22	AAW83354 Human CCR5 protein
8	1841	100.0	352	22	AAW04321 Human chemokine (C
9	1841	100.0	352	23	AAW808343 Human chemokine (C
10	1841	100.0	352	23	AAW52828 Human CC chemokine

11	1841	100.0	439	20	AAW1280 Fusion protein con
12	1836	99.7	371	19	AAW23834 Human CC chemokine
13	1835	99.7	352	22	AAW56342 Non-endogenous hum
14	1835	99.7	352	23	AAW52829 Human CCR5 Gln 55
15	1833	99.6	352	22	AAW07039 Human G-protein ch
16	1833	99.6	352	22	AAW07048 Human G-protein ch
17	1833	99.6	352	22	AAW6858 Human HDGN10 prot
18	1833	99.6	352	23	AAW57152 Human G-protein ch
19	1826	99.2	352	18	AAW07602 Human G-protein ch
20	1826	99.2	352	21	AAW80128 Human G-protein ch
21	1826	99.2	352	22	AAW07037 Human G-protein ch
22	1826	99.2	352	22	AAW07046 Human G-protein ch
23	1826	99.2	352	23	AAW97150 Human G-protein ch
24	1814	98.5	352	22	AAW79089 Amino acid sequenc
25	1807	98.2	352	18	AAW27125 Macaque chemokine
26	1641.5	89.2	332	18	AAW26766 Human chemokine re
27	1546	84.0	354	19	AAW54037 Mouse CC-CR5 prot
28	1365	74.1	360	22	AAW07613 Human CCR2-641 pol
29	1364	74.1	360	16	AAW9166 Human monocyte che
30	1364	74.1	360	18	AAW35833 Human monocyte che
31	1364	74.1	360	22	AAW80108 Human CCR2b protei
32	1364	74.1	360	22	AAW07614 Human Wldd-type CC
33	1358	73.8	360	22	AAW56340 Non-endogenous hum
34	1224	66.5	374	16	AAW9165 Human monocyte che
35	1224	66.5	374	22	AAW60107 Human CCR2a protei
36	1138.5	61.8	329	22	AAW6859 Human MCP-1 recept
37	1055	57.3	355	15	AAW52749 C-C chemokine rece
38	1055	57.3	355	18	AAW26588 Human MIP-1 alpha/R
39	1055	57.3	355	18	AAW25751 Human MIP-1 alpha/R
40	1055	57.3	355	21	AAW30571 Human CC-chemokine
41	1016.5	55.2	355	18	AAW29179 Rat CC chemokine r
42	958	52.0	184	18	AAW27406 Inactive human CCR
43	958	52.0	215	18	AAW27408 HIV-1 co-receptor
44	958	52.0	215	20	AAW8238 Human C-C chemokin
45	942.5	51.2	355	19	AAW51744

ALIGNMENTS

RESULT 1
ID AAW27407 standard; Protein: 352 AA.
XX
AC AAW27407;
XX
DT 14-APR-1998 (first entry)
XX
DE Human CCR5.
XX
KW Human Cys-Cys chemokine receptor 5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder.
XX
OS Homo sapiens.
XX
PN W09732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE00023.
XX
PR 06-AUG-1996; 96EP-0870102.
PR 01-MAR-1996; 96EP-0870021.
XX
PA (EURO-) EUROSCREEN SA.
XX
PI Libert F, Parmentier M, Samson M, Vassart G;
XX WPL: 1997-479829/44.
DR

DR N-PSDB; AAT90117.
 XX Active and inactive forms of human CC chemokine receptor CCR-5 -
 PT useful to diagnose, prevent and/or treat inflammatory disorders,
 PT autoimmune disease and viral infection
 XX
 PS Claim 4; Fig 1b-c; 94pp; English.
 XX
 CC The present sequence is human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES
 CC chemokines, but not by monocyte chemoattractant protein 1 (MCP-1),
 CC MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product
 CC alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of
 CC human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2).
 CC CCR5 or its cDNA can used to diagnose, treat and/or prevent
 CC inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection,
 CC cancer, atherosclerosis and autoimmune disorders.
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 1841; DB 18; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.6e-200;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPLYSVTFEGFGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPLYSVTFEGFGNMLVILLINCKR 60
 QY 61 LKSMTDIYLNLTAISDLFFLLTVPFMAHYAAQMDGNTMCOILTGLYFIFGFSGIFETI 120
 DB 61 LKSMTDIYLNLTAISDLFFLLTVPFMAHYAAQMDGNTMCOILTGLYFIFGFSGIFETI 120
 QY 121 LFTIDRYLAVNAVAFKARVTFGVVTSVTWVAVFAVSLPGIIFTRSQKEGIAHYTCSS 180
 DB 121 LFTIDRYLAVNAVAFKARVTFGVVTSVTWVAVFAVSLPGIIFTRSQKEGIAHYTCSS 180
 QY 181 HPEYSQYQFMKNQTLKIVILGLVPLVWVCISGLTKTLRCRNEKRHRARVRIETI 240
 DB 181 HPEYSQYQFMKNQTLKIVILGLVPLVWVCISGLTKTLRCRNEKRHRARVRIETI 240
 QY 241 MIVYFLFMAVYNIVLLNTFOEFFGLNCCSSNRDLQAMQVETTLGTHCCINPIIYAFV 300
 DB 241 MIVYFLFMAVYNIVLLNTFOEFFGLNCCSSNRDLQAMQVETTLGTHCCINPIIYAFV 300
 QY 301 GEKERNYLVFPOKHIAKRCCKCSIFQOAPERASSVYTRSGEOEISVGL 352
 DB 301 GEKERNYLVFPOKHIAKRCCKCSIFQOAPERASSVYTRSGEOEISVGL 352
 RESULT 2
 AAM27123
 ID AAM27123 standard; protein; 352 AA.
 XX
 AC AAM27123;
 XX
 DT 14-DEC-1997 (first entry)
 XX
 DE Human chemokine receptor 88C.
 XX
 XX Chemokine receptor 88C; atherosclerosis; Rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ligand; modulator; antibody; human.
 XX
 OS Homo sapiens.
 XX
 XX Key location/Qualifiers
 FH 1..32
 FT Domain /label= Extracellular_domain
 FT 56..67
 FT Domain /label= Intracellular_domain

FT Domain 89..112
 FT /label= Extracellular_domain
 FT 125..145
 FT /label= Intracellular_domain
 FT 166..191
 FT /label= Extracellular_domain
 FT 213..235
 FT /label= Intracellular_domain
 FT 259..280
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 FT 301..352
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 PN W09722698-A2.
 PD 26-JUN-1997.
 PF 20-DEC-1996; 96WO-US20759.
 PR 07-JUN-1996; 96US-0661393.
 PR 20-DEC-1995; 95US-0575967.
 PA (ICOS-) ICOS CORP.
 PI Gray PW, Raport CJ, Schweickart VL;
 PI N-PSDB; AAT85161.
 DR WPI: 1997-341689/31.
 DR N-PSDB; AAT85161.
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
 PT to modulate leukocyte trafficking, e.g. for treatment of
 PT inflammation, tumours, viral infections, autoimmune diseases, etc.
 XX
 PS Claim 16; Page 47-48; 65pp; English.
 CC This polypeptide sequence comprises novel human chemokine receptor
 CC 88C, a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a cDNA clone
 CC (AAT85161) isolated from a macrophage library. It shows 62% identity
 CC to CCRX1. Chemokine receptor 88-2B (see AAM27124) has also been
 CC identified. 88C and 88-2B receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides
 CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc.
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 1841; DB 18; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.6e-200;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPLYSVTFEGFGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPLYSVTFEGFGNMLVILLINCKR 60
 QY 61 LKSMTDIYLNLTAISDLFFLLTVPFMAHYAAQMDGNTMCOILTGLYFIFGFSGIFETI 120
 DB 61 LKSMTDIYLNLTAISDLFFLLTVPFMAHYAAQMDGNTMCOILTGLYFIFGFSGIFETI 120
 QY 121 LFTIDRYLAVNAVAFKARVTFGVVTSVTWVAVFAVSLPGIIFTRSQKEGIAHYTCSS 180
 DB 121 LFTIDRYLAVNAVAFKARVTFGVVTSVTWVAVFAVSLPGIIFTRSQKEGIAHYTCSS 180
 QY 181 HPEYSQYQFMKNQTLKIVILGLVPLVWVCISGLTKTLRCRNEKRHRARVRIETI 240
 DB 181 HPEYSQYQFMKNQTLKIVILGLVPLVWVCISGLTKTLRCRNEKRHRARVRIETI 240
 QY 241 MIVYFLFMAVYNIVLLNTFOEFFGLNCCSSNRDLQAMQVETTLGTHCCINPIIYAFV 300

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Db      241 MIVYFLWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVTELTGHTCCINPIYAFV 300
Oy      301 GEFKRNLLVFFOKHIAKRCCKCSIFQOEAPEBASVYTRSTGEDEISVGL 352
Db      301 GEFKRNLLVFFOKHIAKRCCKCSIFQOEAPEBASVYTRSTGEDEISVGL 352

RESULT 3
AAW82335
ID      AAW823835 standard; Protein: 352 AA.
AC      AAW823835;
XX      08-JUN-1998 (first entry)
XX      Human CC chemokine receptor 5 (CCR5).
DE      CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW      human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KM      transgenic animal.
XX      Homo sapiens.
XX      OS
XX      Key
XX      Location/Qualifiers
XX      29..55
XX      /label= I
XX      /note= "transmembrane domain"
XX      109..120
XX      /note= "extracellular loop-1 (Claim 19)"
XX      104..126
XX      /label= III
XX      /note= "transmembrane domain"
XX      143..171
XX      /label= IV
XX      /note= "transmembrane domain"
XX      187..210
XX      /note= "extracellular loop-2 (Claim 19)"
XX      194..219
XX      /label= V
XX      /note= "transmembrane domain"
XX      238..258
XX      /label= VI
XX      /note= "transmembrane domain"
XX      261..276
XX      /note= "extracellular loop-3 (Claim 19)"
XX      277..300
XX      /label= VII
XX      /note= "transmembrane domain"
XX      MO9745543-A2.
XX      04-DEC-1997.
XX      28-MAY-1997; 97WO-US09586.
XX      28-MAY-1996; 96US-0018508.
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX      PI Alkhatib G, Berger EA, Broder CC, Combadiere C;
XX      PI Feng Y, Kennedy PE, Murphy PM;
XX      DR WPI: 1998-032650/03.
XX      DR N-PSDB: AAT76920.
XX      CC Chemokine receptor 5 polypeptide - used to inhibit membrane
XX      fusion between HIV and a target cell
XX      PS Claim 68; Fig 1C; 70pp; English.
XX      CC This protein sequence comprises of a novel human macrophage-selective
XX      CC chemokine receptor that has been designated CCR5. The sequence

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CC      was deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu
CC      variant (see W238340 of CCR5 was also identified. The susceptibility
CC      of human macrophages to HIV infection depends on cell surface
CC      expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane
CC      superfamily of G-protein coupled cell surface molecules. It plays
CC      an essential role in the membrane fusion step of infection by some
CC      HIV isolates. The establishment of stable, non-human cell lines
CC      and transgenic mammals having cells that coexpress human CD4 and
CC      CCR5 provides valuable tools for research of HIV infection.
CC      Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
CC      agents capable of blocking membrane fusion between HIV and target
CC      cells represent potential anti-HIV therapeutics for macrophage
CC      tropic strains of HIV.
XX      Sequence 352 AA;
XX      SQ
XX      Query Match 100.0%; Score 1841; DB 19; Length 352;
XX      Best Local Similarity 100.0%; Pred. No. 3.6e-200;
XX      Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 MDYGVSSPIYDINITYTSEPCKINVKQIARLPLYSLVPIFGFVGMVLIILINCKR 60
Db      1 MDYGVSSPIYDINITYTSEPCKINVKQIARLPLYSLVPIFGFVGMVLIILINCKR 60
Oy      61 LKSMTDIYLLNLAIISDLFELLTPFMAHYAAQMDFGNTMQLLTGLVPIGFPGIFPII 120
Db      61 LKSMTDIYLLNLAIISDLFELLTPFMAHYAAQMDFGNTMQLLTGLVPIGFPGIFPII 120
Oy      121 LITIDRLAVYHNAVFAKARVYTGVTSTVTVVYVAFASIPGIIFTRSQEGILHYCCS 180
Db      121 LITIDRLAVYHNAVFAKARVYTGVTSTVTVVYVAFASIPGIIFTRSQEGILHYCCS 180
Oy      181 HFPYSQYQFKNFQTLKIVILGLVPLLVYICSGILKTLRCRNEKKRRRAVRLFTI 240
Db      181 HFPYSQYQFKNFQTLKIVILGLVPLLVYICSGILKTLRCRNEKKRRRAVRLFTI 240
Oy      241 MIVYFLWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVTELTGHTCCINPIYAFV 300
Db      241 MIVYFLWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVTELTGHTCCINPIYAFV 300
Oy      301 GEFKRNLLVFFOKHIAKRCCKCSIFQOEAPEBASVYTRSTGEDEISVGL 352
Db      301 GEFKRNLLVFFOKHIAKRCCKCSIFQOEAPEBASVYTRSTGEDEISVGL 352

RESULT 4
AAW82332
ID      AAW8232 standard; Protein: 352 AA.
AC      AAW8232;
XX      15-MAR-1999 (first entry)
XX      HIV-1 co-receptor CCR5.
XX      DE HIV-1 co-receptor CCR5.
XX      KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
XX      KW gene therapy; human.
XX      OS Homo sapiens.
XX      Key
XX      Location/Qualifiers
XX      32..56
XX      /note= "transmembrane domain 1"
XX      67..87
XX      /note= "transmembrane domain 2"
XX      101
XX      /note= "transmembrane domain 3"
XX      103..124
XX      /note= "corresponds to TGT (Cy9) in wild-type CCR5,
XX      TGA (Stop) in CCR5m303"
XX      142..167
XX      /note= "transmembrane domain 3"
XX      200..223
XX      /note= "transmembrane domain 4"

```


QY 121 LITIDRYLAVVAVFALKARTVFGVTSVITWVAVFASLPGITFRSKEGLHYTCSS 180
 DB 121 LITIDRYLAVVAVFALKARTVFGVTSVITWVAVFASLPGITFRSKEGLHYTCSS 180
 QY 181 HFPYSOYQFMKNPOTLKIIVILGLVPLLVAVICSGILKTLRCRNEKRRHRAVRLFTI 240
 DB 181 HFPYSOYQFMKNPOTLKIIVILGLVPLLVAVICSGILKTLRCRNEKRRHRAVRLFTI 240
 QY 241 MIVYFLFMAPYNIYLLNTFOEFGLNCCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 DB 241 MIVYFLFMAPYNIYLLNTFOEFGLNCCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 QY 301 GEKFRNLTVEFQKHAKRPFCKCSIFQOEPAPERASSVYTRSTGEDEISVGL 352
 DB 301 GEKFRNLTVEFQKHAKRPFCKCSIFQOEPAPERASSVYTRSTGEDEISVGL 352

RESULT 6
 AAB82948 standard; Protein: 352 AA.
 XX AAB82948;
 XX 21-DEC-2001 (first entry)
 DE Human HIV-1 co-receptor CCR5.
 KM CCR5; chemokine; co-receptor; human immunodeficiency virus type 1;
 KM HIV-1; infection; therapy; vaccine; anti-HIV-1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FH Binding-site 2..18
 PT /note= "binds to HIV-1 gp120"
 XX MO200164710-A2.
 XX 07-SEP-2001.
 PD 28-FEB-2001; 2001MO-US06699.
 XX 28-FEB-2001; 2001MO-US06699.
 PR 29-FEB-2000; 2000US-185667P.
 PR 19-MAY-2000; 2000US-205839P.
 PR 07-FEB-2001; 2001US-267231P.
 XX (PROG-) PROCENICS PHARM INC.
 PA (AAO-) AARON DIAMOND AIDS RES CENT.
 XX Dragic T, Olson WC;
 PI MPI; 2001-611273/70.
 DR N-PSDB; AAB26903.
 XX Novel compounds comprising specific amino acids within CCR5 (HIV 1
 PT co-receptor) amino terminal domain including negatively charged and two
 PT sulfated tyrosine residues is useful for treating HIV infection in
 PT humans
 XX
 PS Claim 1; Page 30; 163pp; English.
 XX The present sequence is that of human HIV-1 co-receptor CCR5.
 CC Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1
 CC gp120-binding site that determines the specificity of the
 CC interaction between CCR5 and HIV-1 gp120. Post-translational
 CC sulfation of the tyrosine residues in the CCR5 N-terminus is
 CC required for gp120 binding and may critically modulate the
 CC susceptibility of target cells to HIV-1 infection in vivo. The
 CC invention provides claimed sulfated peptides (see AAB82947) that
 CC are based on the CCR5 N-terminal region and which are effective
 CC for inhibiting HIV-1 binding to CCR5. These peptides are used in
 CC claimed methods of inhibiting HIV infection of CD4+ cells, of
 CC preventing CD4+ cells from becoming infected with HIV, of treating

CC a subject whose CD4+ cells are infected with HIV, and of
 CC identifying an agent which inhibits binding of a CCR5 ligand to a
 CC CCR5 receptor. The methods may be carried out in a subject,
 CC especially a human, infected (therapeutic method), not infected
 CC with HIV (prophylactic method), or in a subject who is not infected
 CC with, but has been exposed to, HIV.
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 1841; DB 22; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.6e-200;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYGVSSPIVDINITYTSEPCQKINVKQIAARLPLYSIVYFEGVGMVILILNCKR 60
 DB 1 MDYGVSSPIVDINITYTSEPCQKINVKQIAARLPLYSIVYFEGVGMVILILNCKR 60
 QY 61 LKSMTDIYLLNLAISDFELLTVFPMHAYAAQDFGNTMCOQLTGLYFEGSGIFPII 120
 DB 61 LKSMTDIYLLNLAISDFELLTVFPMHAYAAQDFGNTMCOQLTGLYFEGSGIFPII 120
 QY 121 LITIDRYLAVVAVFALKARTVFGVTSVITWVAVFASLPGITFRSKEGLHYTCSS 180
 DB 121 LITIDRYLAVVAVFALKARTVFGVTSVITWVAVFASLPGITFRSKEGLHYTCSS 180
 QY 181 HFPYSOYQFMKNPOTLKIIVILGLVPLLVAVICSGILKTLRCRNEKRRHRAVRLFTI 240
 DB 181 HFPYSOYQFMKNPOTLKIIVILGLVPLLVAVICSGILKTLRCRNEKRRHRAVRLFTI 240
 QY 241 MIVYFLFMAPYNIYLLNTFOEFGLNCCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 DB 241 MIVYFLFMAPYNIYLLNTFOEFGLNCCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 QY 301 GEKFRNLTVEFQKHAKRPFCKCSIFQOEPAPERASSVYTRSTGEDEISVGL 352
 DB 301 GEKFRNLTVEFQKHAKRPFCKCSIFQOEPAPERASSVYTRSTGEDEISVGL 352

RESULT 7
 AAB83354 standard; Protein: 352 AA.
 XX AAB83354;
 XX 09-OCT-2001 (first entry)
 DE Human CCR5 protein sequence.
 KM Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KM human immunodeficiency virus; anti-inflammatory disease; human.
 OS Homo sapiens.
 FH EPI118858-A2.
 PN 25-JUL-2001.
 PD 03-JAN-2001; 2001EP-0300020.
 XX 12-JAN-2000; 2000GB-0000659.
 PR 12-JAN-2000; 2000GB-0000661.
 PR 12-JAN-2000; 2000GB-0000663.
 XX (PRIZ) PRIZER LTD.
 PA (PRIZ) PRIZER INC.
 XX Dobb S, Petros M, Rickelt GA;
 PI MPI; 2001-477088/52.
 DR N-PSDB; AAB87099.
 XX Determining if an agent can modulate CCR5-gp120 interaction, comprises
 PT incubating the agent with CCR5 and gp120 and determining if the agent

PF modulates the interaction
 XX
 PS Claim 1; Page 110; 113pp; English.
 CC This sequence represents the human CCR5 protein sequence.
 CC The invention relates to a method for determining whether an agent is
 CC capable of modulating the interaction of chemotactic chemokine receptor 5
 CC (CCR5) with gpi120, comprising incubating the agent with CCR5 and gpi120
 CC and determining whether the agent modulates the interaction, where gpi120
 CC is associated with CD4, and where the interaction is a low affinity
 CC binding. The method is used to identify an agent capable of modulating
 CC the interaction of CCR5 with gpi120. An agent identified by the method
 CC is used to prepare a pharmaceutical composition for the treatment of a
 CC disease or condition associated with CCR5 and gpi120 interaction, to treat
 CC a subject with a disease or condition associated with CCR5 and gpi120
 CC interaction, and for preparing a pharmaceutical for treating human
 CC immunodeficiency virus (HIV). It can also be used to treat anti-inflammatory
 CC diseases. The method is commercially useful, amenable to high throughput
 CC screening, and detects interaction of gpi120 with cells expressing only
 CC CCR5.
 XX
 SQ Sequence 352 AA:
 Query Match 100.0%; Score 1841; DB 22; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.6e-200;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYVSSPIYDINNTSEPCOKINVKQIARLLPPLYSVFIFGVGNMLVILLINCR 60
 DB 1 MDYVSSPIYDINNTSEPCOKINVKQIARLLPPLYSVFIFGVGNMLVILLINCR 60
 QY 61 LKSMTDIYLLNLAISDLFFLLVFPWAHYAAQWMDGNTMQLTGLYFIFGSGIFETI 120
 DB 61 LKSMTDIYLLNLAISDLFFLLVFPWAHYAAQWMDGNTMQLTGLYFIFGSGIFETI 120
 QY 121 LITIDRYLAVNAVPAKARVTYEGVTSVITWVAVAFSLGIIIFTRQKGLHYTCS 180
 DB 121 LITIDRYLAVNAVPAKARVTYEGVTSVITWVAVAFSLGIIIFTRQKGLHYTCS 180
 QY 181 HPPYSOYQPMKPFQTKIYILGLVPLVMVICSIGILTLRCNREKRRHRAVRLIETI 240
 DB 181 HPPYSOYQPMKPFQTKIYILGLVPLVMVICSIGILTLRCNREKRRHRAVRLIETI 240
 QY 241 MIVYFLFMAPYNIIVLLNTFOEFGIINCCSSNRDQAMQVETLTGTHCCINPIIYAV 300
 DB 241 MIVYFLFMAPYNIIVLLNTFOEFGIINCCSSNRDQAMQVETLTGTHCCINPIIYAV 300
 QY 301 GEKFRNYLVFPQKHAKRFCKCSIFQOEAPEBRASSVYTRSGEOEISVGL 352
 DB 301 GEKFRNYLVFPQKHAKRFCKCSIFQOEAPEBRASSVYTRSGEOEISVGL 352
 RESULT 8
 AAEO4321
 ID AAEO4321 standard; Protein; 352 AA.
 AC AAEO4321:
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human chemokine receptor (CCR), CC-CR-5 related protein #2.
 XX
 KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immunodeficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CR-5; envelope glycoprotein; anti-HIV.
 XX
 OS Homo sapiens.
 XX
 PN US6258527-B1.
 XX
 PD 10-JUL-2001.
 XX

PF 21-MAY-1997; 97US-0861105.
 XX
 PR 20-MAY-1996; 96US-0017157.
 PR 19-JUN-1996; 96US-0020043.
 PR 19-MAY-1997; 97US-0838660.
 PA (AAEO-) AARON DIAMOND AIDS RES CENT.
 PA (UWNY) UNIV NEW YORK STATE.
 XX
 PI Littman DR, Deng H, Elmler W, Landau NR, Liu R;
 XX
 DR WPI; 2001-417127/44.
 DR N-PSDB; AAD08577.
 XX
 PS Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 PT HIV -
 XX
 CC Disclosure; Column 47-50; 37pp; English.
 CC
 CC The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immunodeficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a
 CC human chemokine receptor (CCR) where the CD4 and the CCR are present on
 CC the cell surface of transformed mammalian cell. The invention is useful
 CC for identifying drugs or antibodies that interfere with the
 CC translocation of HIV into transformed mammalian cell or for identifying
 CC a human chemokine receptor that facilitates the infection of a
 CC particular HIV strain into the transformed mammalian cell. Compounds
 CC identified can be used to treat cellular dysfunction and to prevent or
 CC combat HIV infection. The present sequence is a human chemokine receptor
 CC (CCR), CC-CR-5 related protein. CC-CR-5 is the principal cofactor for
 CC entry mediated by the envelope glycoproteins of primary macrophage-tropic
 CC strains of HIV-1.
 XX
 SQ Sequence 352 AA:
 Query Match 100.0%; Score 1841; DB 22; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.6e-200;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDYVSSPIYDINNTSEPCOKINVKQIARLLPPLYSVFIFGVGNMLVILLINCR 60
 DB 1 MDYVSSPIYDINNTSEPCOKINVKQIARLLPPLYSVFIFGVGNMLVILLINCR 60
 QY 61 LKSMTDIYLLNLAISDLFFLLVFPWAHYAAQWMDGNTMQLTGLYFIFGSGIFETI 120
 DB 61 LKSMTDIYLLNLAISDLFFLLVFPWAHYAAQWMDGNTMQLTGLYFIFGSGIFETI 120
 QY 121 LITIDRYLAVNAVPAKARVTYEGVTSVITWVAVAFSLGIIIFTRQKGLHYTCS 180
 DB 121 LITIDRYLAVNAVPAKARVTYEGVTSVITWVAVAFSLGIIIFTRQKGLHYTCS 180
 QY 181 HPPYSOYQPMKPFQTKIYILGLVPLVMVICSIGILTLRCNREKRRHRAVRLIETI 240
 DB 181 HPPYSOYQPMKPFQTKIYILGLVPLVMVICSIGILTLRCNREKRRHRAVRLIETI 240
 QY 241 MIVYFLFMAPYNIIVLLNTFOEFGIINCCSSNRDQAMQVETLTGTHCCINPIIYAV 300
 DB 241 MIVYFLFMAPYNIIVLLNTFOEFGIINCCSSNRDQAMQVETLTGTHCCINPIIYAV 300
 QY 301 GEKFRNYLVFPQKHAKRFCKCSIFQOEAPEBRASSVYTRSGEOEISVGL 352
 DB 301 GEKFRNYLVFPQKHAKRFCKCSIFQOEAPEBRASSVYTRSGEOEISVGL 352
 RESULT 9
 ABB08343
 ID ABB08343 standard; Protein; 352 AA.
 AC ABB08343:
 XX
 PD ABB08343;
 XX

DT 18-JUN-2002 (first entry)

XX Human chemokine (C-C motif) receptor 5 polypeptide.

XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;

KM single nucleotide polymorphism; SNP; human immunodeficiency virus 1;

KM HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;

KM genotype; polymorphic variant; transgenic; drug screening; gene therapy;

XX chromosome 3p21.

OS Homo sapiens.

XX Key Location/Qualifiers

PH MISC-difference 55 /label= Leu, Gln

FT MISC-difference 182 /label= Phe, Leu

FT MISC-difference 223 /label= Arg, Gln

FT MISC-difference 223 /label= Arg, Gln

XX MO200177125-A2.

XX 18-OCT-2001.

XX 04-APR-2001; 2001WO-US10708.

XX 05-APR-2000; 2000US-194361P.

XX (GENA-) GENA155ANCE PHARM INC.

XX Chot JY, Klem SE, Koshy B;

XX WPI: 2002-041282/05.

DR N-PSDB: ABA97318, ABA97319.

XX New haplotypes of the human chemokine (C-C motif) receptor 5 gene,

PT useful to diagnose and treat diseases associated with its abnormal

PT expression or function, including human immunodeficiency virus-1

PT infection -

XX Claim 29: Fig 3; 61pp; English.

XX The present sequence is that of a polypeptide encoded by the human

CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see

CC ABA97318, ABA97319). The specification describes haplotyping the CCR5

CC gene of an individual by determining if the individual has one of the

CC CCR5 haplotypes or haplotype pairs fully defined in the specification.

CC The specification also describes an isolated polynucleotide comprising a

CC nucleotide sequence which is a polymorphic variant of the reference CCR5

CC gene sequence and comprises an isogene defined by a haplotype described

CC in the specification and its encoded polypeptide. The methods of the

CC invention are useful to diagnose and develop treatment for diseases

CC associated with abnormal expression or function of the gene. The CCR5

CC isogenes and the screened compounds are useful for treating human

CC immunodeficiency virus (HIV)-1 infection and the progression to acquired

CC immunodeficiency syndrome (AIDS). The invention has antiviral

CC applications. The specification describes genotyping the CCR5 gene of an

CC individual; predicting a haplotype pair for the CCR5 gene of an

CC individual; identifying an association between a trait and a haplotype or

CC haplotype pair of the CCR5 gene. The specification describes a CCR5

CC composition comprising a genotyping oligonucleotide for detecting a CCR5

CC polymorphism; a recombinant non-human organism transformed with CCR5

CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;

CC an isolated antibody specific for the CCR5 polypeptide and a method for

CC screening drugs targeting the CCR5 polypeptide.

XX Sequence 352 AA:

SO Query Match 100.0%; Score 1841; DB 23; Length 352;

Best Local Similarity 100.0%; Pred. No. 3.6e-200;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLVSLVIFGFGNMLVILLINCKR 60

DB 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLVSLVIFGFGNMLVILLINCKR 60

OY 61 LKSMTDIYILMLAISDLFFLLTPVFMAYAAQDFGNTMQLTGLYFIFGFSIGIFPII 120

DB 61 LKSMTDIYILMLAISDLFFLLTPVFMAYAAQDFGNTMQLTGLYFIFGFSIGIFPII 120

OY 121 LKTDIDYLAHVAVFALKARTVTGVTSVITWVAVPASLPGIIFTRSOEGLYHTCSS 180

DB 121 LKTDIDYLAHVAVFALKARTVTGVTSVITWVAVPASLPGIIFTRSOEGLYHTCSS 180

OY 181 HEPYSQYQFMNFTLKIIVIGLVPLVPMVYICSGILKTLRCNEKRRRAVRLIPTI 240

DB 181 HEPYSQYQFMNFTLKIIVIGLVPLVPMVYICSGILKTLRCNEKRRRAVRLIPTI 240

OY 241 MIVYELFAPYNIYLLNTFOEFGNLNCSNNRDMOAMOTETLGMTHCCINPIYAFV 300

DB 241 MIVYELFAPYNIYLLNTFOEFGNLNCSNNRDMOAMOTETLGMTHCCINPIYAFV 300

OY 301 GEFERNYLLVFEQKHIAKRFCKCSIFQOEAPEKASSVYTRSTGBOEISVGL 352

DB 301 GEFERNYLLVFEQKHIAKRFCKCSIFQOEAPEKASSVYTRSTGBOEISVGL 352

RESULT 10

AAM52828

ID AAM52828 standard; Protein: 352 AA.

XX AAM52828;

XX 22-FEB-2002 (first entry)

XX Human CC chemokine receptor 5 (CCR5).

XX CCR5; CC chemokine receptor 5; human; HIV infection;

KM human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;

KM drug screening; identification.

OS Homo sapiens.

XX WO200171346-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09155.

XX 21-MAR-2000; 2000US-190946P.

PR 21-MAR-2000; 2000US-190946P.

PR 21-MAR-2000; 2000US-191299P.

PR 20-MAR-2001; 2001US-0813448.

PR 20-MAR-2001; 2001US-0813651.

PR 20-MAR-2001; 2001US-0813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehlr CA;

PI WPI: 2002-010610/01.

DR N-PSDB: ABA02317.

XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,

PT comprises binding a molecule from library to a molecule having binding

PT property corresponding to CCR5 and identifying bound molecule -

XX Example 3: Fig 4A: 50pp; English.

XX The invention relates to a method for identifying a binding compound

CC for CC chemokine receptor 5 (CCR5). The method involves screening a

CC library of test molecules (particularly peptides) with immobilized CCR5,

CC and then identifying those molecules which bind. The invention also

CC relates to CCR5-binding molecules identified using the method of the

CC invention, a transfer vector encoding consensus motifs for CCR5-binding

CC peptides, a transfer vector encoding tagged CCR5, a computer-aided


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XX OS Homo sapiens.
XX Key Location/Qualifiers
FH Key 48..74
FT Domain /label-1
FT /note="transmembrane domain"
FT 123..145
FT /label-III
FT /note="transmembrane domain"
FT 162..190
FT /label-IV
FT /note="transmembrane domain"
FT 213..238
FT /label-V
FT /note="transmembrane domain"
FT 257..277
FT Domain /label-VI
FT /note="transmembrane domain"
FT 296..319
FT /label-VII
FT /note="transmembrane domain"
XX PN K09745543-A2.
XX 04-DEC-1997.
XX 28-MAY-1997; 97MO-US09586.
XX 28-MAY-1996; 96US-0018508.
XX (US98 ) US DEPT HEALTH & HUMAN SERVICES.
XX Alkhalib G, Berger EA, Broder CC, Combadiere C;
XX Feng Y, Kennedy PE, Murphy PM;
XX WPI; 1998-032650/03.
XX N-PSDB; AAT76919.
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane
XX fusion between HIV and a target cell
XX Example 1; Fig 1B; 70pp; English.
XX This protein sequence comprises an A1a127Leu variant of a novel
XX human macrophage-selective CC chemokine receptor (see also
XX AAW23835) that has been designated CCR5. The sequence was deduced
XX from an isolated cDNA clone (see AAT76919). The conservative
XX variation should not affect the activity of CCR5. The susceptibility
XX of human macrophages to HIV infection depends on cell surface
XX expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane
XX superfamily of G-protein coupled cell surface molecules. It plays
XX an essential role in the membrane fusion step of infection by some
XX HIV isolates. The establishment of stable, non-human cell lines
XX and transgenic mammals having cells that coexpress human CD4 and
XX CCR5 provides valuable tools for research of HIV infection.
XX Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX agents capable of blocking membrane fusion between HIV and target
XX cells represent potential anti-HIV therapeutics for macrophage
XX tropic strains of HIV.
SQ Sequence 371 AA;
Query Match 99.7%; Score 1836; DB 19; Length 371;
Best Local Similarity 99.7%; Pred. No. 1.4e-199;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MDVQSSPIYDINTYSEPCOKINVKOIAARLPLPLSLVFIFGVGNMLVILINCKR 60
DB 20 MDVQSSPIYDINTYSEPCOKINVKOIAARLPLPLSLVFIFGVGNMLVILINCKR 79
OY 61 LKSWTDIYLNLAIISDLFELLTPFMAHYLAQMDFGNTMCCOLLTGIFYGFSGIFPII 120

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DB 80 LKSWTDIYLNLAIISDLFELLTPFMAHYLAQMDFGNTMCCOLLTGIFYGFSGIFPII 139
OY 121 LITIDRYLAVYHVAFAKARTVTEGVTSVITVWVAFAAPLGIIFTRSGEGHYTCSS 180
DB 140 LITIDRYLAVYHVAFAKARTVTEGVTSVITVWVAFAAPLGIIFTRSGEGHYTCSS 199
OY 181 HEPYSQYQFMKNFOTLKIIVILGLVPLLVNVCYSGILKTLRCRNEKKRRRAVRLIFTI 240
DB 200 HEPYSQYQFMKNFOTLKIIVILGLVPLLVNVCYSGILKTLRCRNEKKRRRAVRLIFTI 259
OY 241 MIYVFLWAPRYNIVLLNTQEFEGGLNCCSSNNLDQAMQVETLGTHTCCINPIYAFV 300
DB 260 MIYVFLWAPRYNIVLLNTQEFEGGLNCCSSNNLDQAMQVETLGTHTCCINPIYAFV 319
OY 301 GEKFRNTLVFQKHAKRRCCKCSIFQOEAPEPAASSVYTRSGEISVGL 352
DB 320 GEKFRNTLVFQKHAKRRCCKCSIFQOEAPEPAASSVYTRSGEISVGL 371
RESULT 13
ABB56342
ID ABB56342 standard; Protein: 352 AA.
XX AC ABB56342;
XX 18-FEB-2002 (first entry)
XX DE Non-endogenous human GPCR protein, SEQ ID NO: 477.
XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
XX constitutively activated GPCR; agonist; disease.
XX OS Homo sapiens.
XX Synthetic.
XX PN W0200177172-A2.
XX 18-OCT-2001.
XX 05-APR-2001; 2001MO-US11098.
XX 07-APR-2000; 2000US-195747P.
XX (AREN-) ARENA PHARM INC.
XX PI Lehmann-Brulmsma K, Llaw CW, Lin I;
XX WPI; 2001-648758/74.
XX N-PSDB; ABI97978.
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX disease treatment, comprises contacting candidate compounds with
XX versions of GPCRs -
XX Claim 1; Page 277-278; 394pp; English.
XX The invention relates to G protein-coupled receptors (GPCRs) for which
XX the endogenous ligand has been identified. Non-endogenous GPCRs
XX constitutively activated versions of known GPCRs are used in the
XX invention for the direct identification of candidate compounds as
XX receptor agonists, inverse agonists or partial agonists. Such
XX agonists are useful as therapeutic agents for diseases or disorders
XX associated with GPCRs. The present sequence is a non-endogenous
XX version of a known human GPCR.
SQ Sequence 352 AA;
Query Match 99.7%; Score 1835; DB 22; Length 352;
Best Local Similarity 99.7%; Pred. No. 1.7e-199;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MDVQSSPIYDINTYSEPCOKINVKOIAARLPLPLSLVFIFGVGNMLVILINCKR 60

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Db      1 MDYVSSPIYDINYYTSEPCQKINVKQIARLLPPLYSVIFGFGVGNMLVILLINCKR 60
QY      LKSMTDIYLLNLAISDLFFLLTVPPMAHYAAQMPGNTMCOLLGLYIFGFGSGLFFII 120
Db      61 LKSMTDIYLLNLAISDLFFLLTVPPMAHYAAQMPGNTMCOLLGLYIFGFGSGLFFII 120
QY      121 LTTIDRYLAHVAVALKARVTFGVVTSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
Db      121 LTTIDRYLAHVAVALKARVTFGVVTSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
QY      161 HPPYSQYQFQWKNFQTLKIYILGLVPLVMVTCYSGILKTLRCRNEKKRHAVALRIIFTI 240
Db      161 HPPYSQYQFQWKNFQTLKIYILGLVPLVMVTCYSGILKTLRCRNEKKRHAVALRIIFTI 240
QY      241 MIVYFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLDAQVETLGMTHCCINPIITIAV 300
Db      241 MIVYFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLDAQVETLGMTHCCINPIITIAV 300
QY      301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352
Db      301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352

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RESULT 14
AAM52829
ID      AAM52829 standard; Protein; 352 AA.
XX
AC      AAM52829;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Human CCR5 Gln 55 variant.
XX
KW      CCR5; CC chemokine receptor 5; human; HIV infection;
KW      human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KW      drug screening; identification; variant.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      Misc-difference 55 /note= "Glu replaces wild-type Leu; encoded by CTG"
FT      Misc-difference 58 /note= "Encoded by AGC"
FT
XX
PD      WO200171346-A2.
XX
XX      27-SEP-2001.
XX
XX      21-MAR-2001; 2001WO-US09155.
XX
XX      21-MAR-2000; 2000US-190946P.
XX      21-MAR-2000; 2000US-190946P.
XX      21-MAR-2000; 2000US-191299P.
XX      20-MAR-2001; 2001US-0813448.
XX      20-MAR-2001; 2001US-0813651.
XX      20-MAR-2001; 2001US-0813653.
XX
XX      (CONS-) CONSENSUS PHARM INC.
XX
XX      Nestor JJ, Wilson CT, See RH, Tan Hehr CA;
XX
XX      WPI; 2002-010610/01.
XX      N-PSDB; ABA02318.
XX
XX      Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX      comprises binding a molecule from library to a molecule having binding
XX      property corresponding to CCR5 and identifying bound molecule
XX
XX      Example 3; Fig 4B; 50pp; English.
XX
XX      The invention relates to a method for identifying a binding compound
XX      for CC chemokine receptor 5 (CCR5). The method involves screening a

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CC      library of test molecules (particularly peptides) with immobilised CCR5,
CC      and then identifying those molecules which bind. The invention also
CC      relates to CCR5-binding molecules identified using the method of the
CC      invention, methods for identifying consensus motifs for CCR5-binding
CC      peptides, a transfer vector encoding tagged CCR5, a computer-aided
CC      methods for determining the relative binding affinity of a test molecule
CC      to CCR5 and a computer aided drug screening assay that utilises the
CC      three-dimensional structure of CCR5. Compounds identified using the
CC      methods of the invention are useful for treating or preventing HIV
CC      (human immunodeficiency virus) infection or AIDS (acquired
CC      immunodeficiency syndrome) in a patient. The methods of the invention
CC      may also be used to identify agonists or antagonists of the interaction
CC      of CCR5 with its natural ligand, and to determine a binding motif for
CC      CCR5. The present sequence represents a naturally occurring variant of
CC      human CCR5 in which there is a glutamine, rather than a leucine, at
CC      position 55.
SQ      Sequence 352 AA:

```

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Query Match          99.7%; Score 1835; DB 23; Length 352;
Best Local Similarity 99.7%; Pred. No. 1,7e-199;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MDYVSSPIYDINYYTSEPCQKINVKQIARLLPPLYSVIFGFGVGNMLVILLINCKR 60
Db      1 MDYVSSPIYDINYYTSEPCQKINVKQIARLLPPLYSVIFGFGVGNMLVILLINCKR 60
QY      61 LKSMTDIYLLNLAISDLFFLLTVPPMAHYAAQMPGNTMCOLLGLYIFGFGSGLFFII 120
Db      61 LKSMTDIYLLNLAISDLFFLLTVPPMAHYAAQMPGNTMCOLLGLYIFGFGSGLFFII 120
QY      121 LTTIDRYLAHVAVALKARVTFGVVTSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
Db      121 LTTIDRYLAHVAVALKARVTFGVVTSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
QY      161 HPPYSQYQFQWKNFQTLKIYILGLVPLVMVTCYSGILKTLRCRNEKKRHAVALRIIFTI 240
Db      161 HPPYSQYQFQWKNFQTLKIYILGLVPLVMVTCYSGILKTLRCRNEKKRHAVALRIIFTI 240
QY      181 HPPYSQYQFQWKNFQTLKIYILGLVPLVMVTCYSGILKTLRCRNEKKRHAVALRIIFTI 240
Db      181 HPPYSQYQFQWKNFQTLKIYILGLVPLVMVTCYSGILKTLRCRNEKKRHAVALRIIFTI 240
QY      241 MIVYFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLDAQVETLGMTHCCINPIITIAV 300
Db      241 MIVYFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLDAQVETLGMTHCCINPIITIAV 300
QY      301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352
Db      301 GEKFRNYLLVFPQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352

```

```

RESULT 15
AAE07039
ID      AAE07039 standard; Protein; 352 AA.
XX
AC      AAE07039;
XX
DT      16-OCT-2001 (first entry)
XX
DE      Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX
XX      Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
XX      human immunodeficiency virus; antimitochondrial; vasodilator; vulnery;
XX      cytoskeletal; immunosuppressive; neotropic; neuroprotective; gene therapy;
XX      neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
XX      rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
XX      gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
XX      haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
XX      multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
XX      cardiovascular disorder; myocardial ischaemia.
XX
XX      Homo sapiens.
XX
XX      WO200158915-A2.
XX
XX      16-AUG-2001.
PD

```

XX 09-FEB-2001; 2001WO-US04152.
PF
PR 09-FEB-2000; 2000US-0181258.
PR 09-MAR-2000; 2000US-0187999.
PR 22-SEP-2000; 2000US-0234336.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI: 2001-488965/53.
DR N-PSDB: AAD13198.
XX
PT Isolated nucleic acid encoding a human G-protein chemokine receptor
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating
PT autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
PT disorders and neurodegenerative disorders -
XX
PS
PS Example 40: Page 486-487; 495pp; English.

XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing
CC or ameliorating a disease or disorder associated with inflammation,
CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
CC aberrant T-cell antigen presenting cell interaction. The disease or
CC disorder may also be an infectious disease (e.g. a viral infection such
CC as an early stage HIV infection, a cytomegalovirus infection, or a
CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
CC a neurodegenerative disorder. The disease or disorder may be associated
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
CC is used as a food additive or preservative to increase or decrease
CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
CC antibodies, agonists and antagonists are also useful in the
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
CC hemolytic anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis); cardiovascular disorders (myocardial ischemias) and
CC wound healing.
XX
XX

SO Sequence 352 AA;

Query Match 99.68; Score 1833; DB 22; Length 352;
Best Local Similarity 99.78; Pred. No. 2,9e-199;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYYTSEPOKINVKQIAARLLPPLYSVPIFGVGNMLYILINCKR 60
DB 1 MDYOVSSPIYDINYYTSEPOKINVKQIAARLLPPLYSVPIFGVGNMLYILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFETI 120
DB 61 LKSMTDIYLLNLAIISDLFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFETI 120
QY 121 LTTDRILAVVHANFALKARTVTVGVTSVTWVAVFASLPGIIFTRSOKEGLHYTCSS 180
DB 121 LTTDRILAVVHANFALKARTVTVGVTSVTWVAVFASLPGIIFTRSOKEGLHYTCSS 180
QY 181 HFPYSOYQFMNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKKRRHARVLIPTI 240
DB 181 HFPYSOYQFMNFQTLKIVILGLVPLLVWVICYSGILKTLRCRNEKKRRHARVLIPTI 240
QY 241 MIVFLFWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINDPIYAFV 300
DB 241 MIVFLFWAPYNIYLLNTFOEFFGLNCCSSNRLDQAMQVETLGMTHCCINDPIYAFV 300
QY 301 GEFKRNILVFFOKHIAKRCCKCSIFQOAPERASSVYTRSTEGOEISVGL 352
DB 301 GEFKRNILVFFOKHIAKRCCKCSIFQOAPERASSVYTRSTEGOEISVGL 352

DB 301 GEFKRNILVFFOKHIAKRCCKCSIFQOAPERASSVYTRSTEGOEISVGL 352

Search completed: June 3, 2003, 15:19:02
Job time : 66.5644 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 3, 2003, 15:16:36 ; Search time 32.2822 Seconds

(without alignments)
1048.235 Million cell updates/sect

Title: US-09-939-226-5

Perfect score: 1841

Sequence: 1 MDYQVSSPIYDINVTSEPC.....ERASSVYTRSTGEQISVGL 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.*
2: PIR.*
3: PIR.*
4: PIR.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1841	100.0	352	2 A43113	Chemokine (C-C) re
2	1364	74.1	360	2 JC2443	Chemokine (C-C) re
3	1224	66.5	374	2 I38450	Chemokine (C-C) re
4	1055	57.3	355	2 A45177	Chemokine (C-C) re
5	1007.5	54.7	355	2 I49339	macrophage Inflamm
6	1001.5	54.4	359	2 I49341	MIP-1 alpha recept
7	935.5	50.8	355	2 G02436	Chemokine (C-C) re
8	919	49.9	360	2 A57160	Chemokine (C-C) re
9	906	49.2	360	2 JC4587	Chemokine (C-C) re
10	829	45.0	383	2 S55594	G protein-coupled
11	799.5	43.4	356	2 I49340	MIP-1 alpha recept
12	746.5	40.5	355	2 JC5067	G protein-coupled
13	712	38.7	354	2 I58186	probable G protein
14	673	36.6	344	2 JC5942	Chemokine receptor
15	670.5	36.4	355	2 JC4304	orphan G protein-c
16	567	30.8	378	2 B55735	Lymphocyte-specifi
17	562	30.5	378	2 A55735	G protein-coupled
18	559	30.4	369	2 JC5068	G protein-coupled
19	553	30.0	378	2 A45680	G protein-coupled
20	541	29.4	333	2 I65989	G protein-coupled
21	521	28.3	360	2 A53611	Interleukin-8 rece
22	517.5	28.1	359	2 A48921	Interleukin-8 rece
23	515	28.0	355	2 J01231	Interleukin-8 rece
24	514.5	27.9	358	2 A53752	Interleukin-8 rece
25	510.5	27.7	367	2 J00349	Interferon-Inducib
26	509.5	27.7	350	2 JN0621	G protein-coupled
27	506.5	27.5	350	2 A39445	Interleukin-8 rece
28	506	27.5	352	2 G00048	fusin (LPSRA) - C
29	506	27.5	352	2 A45747	neuropeptide Y/pep

30	496.5	27.0	353	2 S28787	neuropeptide Y/pep
31	490.5	26.6	356	2 S42096	Interleukin-8 rece
32	474.5	25.8	359	2 JC2134	angiotensin II rec
33	473.5	25.7	359	2 A42656	angiotensin II rec
34	472	25.6	374	2 S42628	G protein-coupled
35	471	25.6	359	2 I51372	angiotensin II rec
36	469.5	25.5	359	2 JH0621	angiotensin II rec
37	468.5	25.4	359	2 S44425	angiotensin II rec
38	468.5	25.4	359	2 JC1194	angiotensin II rec
39	466.5	25.3	359	2 S15403	angiotensin II rec
40	464.5	25.2	359	2 J01516	angiotensin II rec
41	461.5	25.1	359	2 JC1104	angiotensin II rec
42	461	25.0	327	2 S56162	MCRI5 protein - h
43	461	25.0	372	2 S26667	G protein-coupled
44	460.5	25.0	359	2 A48857	angiotensin II rec
45	453	24.6	374	2 S32785	G protein-coupled

ALIGNMENTS

RESULT 1
A43113
Chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C>Date: 12-Jul-1996 #sequence, revision 12-Jul-1996 #text, change 20-Jun-2000
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A>Title: Molecular cloning and functional expression of a new human CC-chemokine rece
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X51492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Lisnard, C.; Farber, C.M.; Sarag
M.; Imbl, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;
Nature 382, 722-725, 1996
A>Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206;207-230 <SAM2>
A:Accession: A58834
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, IKDSHGAGPAACGHLILGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X93933; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A>Note: this frameshift mutation results in a non-functional receptor but confers a d
R may have had a selective advantage by conferring resistance to Yersinia plague inf
R:Combadere, C.; Ahuja, S.K.; Tiffeny, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A>Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AB17071.1; PID:g1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'V', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A>Title: Molecular cloning and functional characterization of a novel human CC chemok
A:Reference number: A58833; MUID:96291862; PMID:8663314

A:Accession: A58833
 A:Molecule type: mRNA
 A:Residues: 1-352 <RAP>
 A:Cross-references: GB:U54994; NID:91457945; PIDN:AAC050598.1; PID:91457946
 C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C:Genetics:
 A:Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
 A:Cross-references: GDB:1230510; OMIM:601373
 A:Map position: 3p21-3p21
 C:Function:
 A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
 A:Note: probably acts to control granulocyte proliferation and differentiation
 C:Superfamily: Vertebrate rhodopsin
 C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
 F:32-56/Domain: transmembrane #status predicted <TM1>
 F:67-87/Domain: transmembrane #status predicted <TM2>
 F:103-124/Domain: transmembrane #status predicted <TM3>
 F:142-166/Domain: transmembrane #status predicted <TM4>
 F:193-218/Domain: transmembrane #status predicted <TM5>
 F:236-257/Domain: transmembrane #status predicted <TM6>
 F:285-300/Domain: transmembrane #status predicted <TM7>
 F:20-269,101-178/Disulfide bonds: #status predicted
 F:268/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:336/337,342/Binding site: phosphate (Ser) (covalent) #status predicted
 F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 1841; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 7,5e-145;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDQVSSPIYDINTYSEPCOKINVKQIARLLPLYSLVTFGVGMVLIIINCKR 60
 DB 1 MDQVSSPIYDINTYSEPCOKINVKQIARLLPLYSLVTFGVGMVLIIINCKR 60
 QY 61 LKSMIDYILNLAISDDEFLITVPFWAHAAQMGNTMQLLGLYIFGSSGIFPII 120
 DB 61 LKSMIDYILNLAISDDEFLITVPFWAHAAQMGNTMQLLGLYIFGSSGIFPII 120
 QY 121 LITDRYLAHVAVPALAKARTVFGVTSVTWVAVAVASLPGLIIFTRSGKGLHYTCSS 180
 DB 121 LITDRYLAHVAVPALAKARTVFGVTSVTWVAVAVASLPGLIIFTRSGKGLHYTCSS 180
 QY 181 HEPYSQYQFWMKQFQIKIIVIGLVPLLMVTCYSGILKTLRCRNEKRRAVRLIFTI 240
 DB 181 HEPYSQYQFWMKQFQIKIIVIGLVPLLMVTCYSGILKTLRCRNEKRRAVRLIFTI 240
 QY 241 MIVYFLFAPRYIVILLNTFOEFGLNCCSSNRDQAMQVETLGMTHCCINPIIYAFV 300
 DB 241 MIVYFLFAPRYIVILLNTFOEFGLNCCSSNRDQAMQVETLGMTHCCINPIIYAFV 300
 QY 301 GEKFNYYLTFPOKHIAKFCCKCSIFQOEAPEERASSYTRSTGEQEISVGL 352
 DB 301 GEKFNYYLTFPOKHIAKFCCKCSIFQOEAPEERASSYTRSTGEQEISVGL 352

RESULT 2

JC2443
 chemokine (C-C) receptor 2, splice form B - human
 N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
 C:Species: Homo sapiens (man)
 C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C:Accession: JC2443; I38463
 R:Chang, I.F.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
 A:Reference number: JC2443; MUID:9432942; PMID:8048929
 A:Accession: JC2443
 A:Molecule type: mRNA
 A:Residues: 1-360 <YAM>
 A:Cross-references: DDBJ:D29984; NID:9531246; PIDN:BA06253.1; PID:9531247
 R:Chao, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A:Title: Molecular cloning and functional expression of two monocyte chemoattractant
 A:Reference number: A53477; MUID:94195821; PMID:8146186
 A:Accession: I38463
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-360 <RES>
 A:Cross-references: EMBL:U03905; NID:9472557; PIDN:AAA19120.1; PID:9472558
 C:Genetics:
 A:Gene: GDB:CMKBR2
 A:Cross-references: GDB:337364; OMIM:601267
 A:Map position: 3p21-3p21
 C:Superfamily: Vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr
 F:43-70/Domain: transmembrane #status predicted <TM1>
 F:81-100/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:207-226/Domain: transmembrane #status predicted <TM5>
 F:244-268/Domain: transmembrane #status predicted <TM6>
 F:287-309/Domain: transmembrane #status predicted <TM7>
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:113-190/Disulfide bonds: #status predicted

Query Match 74.1%; Score 1364; DB 2; Length 360;
 Best Local Similarity 75.5%; Pred. No. 2.1e-105;
 Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

QY 10 YQINVTSPCOKINVKQIARLLPLYSLVTFGVGMVLIIINCKRLKSMIDYIL 69
 DB 24 FYDYD--GAPCKRFDYQKQGAQLPLPLYSLVTFGVGMVLIIINCKRLKCLTDYIL 81
 QY 70 LNAISDDEFLITVPFWAHAAQMGNTMQLLGLYIFGSSGIFPIIILITDRYLA 129
 DB 82 LNAISDDEFLITPLMAASANEWFVGNAMCKLFGVHIGYFGSIFPIIILITDRYLA 141
 QY 130 VYHAFALAKARTVFGVTSVTWVAVAVASLPGLIIFTRSGKGLHYTCSSHEPPYSQYF 189
 DB 142 IVHAFALAKARTVFGVTSVTWVAVAVASLPGLIIFTRSGKGLHYTCSSHEPPYSQYF 197
 QY 190 MNFQRLKIVIGLVPLLMVTCYSGILKTLRCRNEKRRAVRLIFTIMIVFLFWA 249
 DB 198 MNFQRLKIVIGLVPLLMVTCYSGILKTLRCRNEKRRAVRLIFTIMIVFLFWA 257
 QY 250 PYNIVLLNTFOEFGLNCCSSNRDQAMQVETLGMTHCCINPIIYAFVGEKERNYLL 309
 DB 258 PYNIVLLNTFOEFGLNCCSSNRDQAMQVETLGMTHCCINPIIYAFVGEKERNYLL 317
 QY 310 VFFQKHIAKFCCKCSIFQOEAPEERASSYTRSTGEQEISVGL 352
 DB 318 VFFQKHIAKFCCKCSIFQOEAPEERASSYTRSTGEQEISVGL 360

RESULT 3

I38450
 chemokine (C-C) receptor 2, splice form A - human
 N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte c
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
 C:Accession: I38450
 R:Chao, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A:Title: Molecular cloning and functional expression of two monocyte chemoattractant
 A:Reference number: A53477; MUID:94195821; PMID:8146186
 A:Accession: I38450
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <RES>
 A:Cross-references: EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:9472556
 C:Genetics:
 A:Gene: GDB:CMKBR2
 A:Cross-references: GDB:337364; OMIM:601267
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin

C:Genetics:
A:Gene: GDB:CMKR1; CMKR-1
A:Cross-references: GDB:138446; OMIM:601159
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

[illegible]

```

OY 190 WKNFOTKIVIGVLPRLVMYICVSGIKTLRCNEKKRHHAVLPIFMIVUFLFEMA 249
    | | | | : | | | | | | | | | | : | | | | | | | | | |
Db 195 WKRFQALKNLGLLPLRLVMYITTCAGIIRILRL -RPSEKVAAYVRLIRATITLLEPLMWT 253
OY 250 PYNIALLNTFOEFGJLNNCCSSNNRDLQAMQVLETIGMHCNCINPIITVAVGEKFRNYLL 309
    | | | : : | | | | | | | | | | | | | | | | | | | | |
Db 254 PYNLVSFSAFQDVLFTNOCQESKHLDLAMQVTEVATYATRHCCVNPITITVFGGERFKYLR 313
OY 310 VFOFKHAKRFQCCSIFEOEAERBASVYTRSTBOEISV 351
    | | | | : | | | | | | | | | | | | | | | |
Db 314 QLFQRBHVALPLAKMLPFLSVDLERKSSI -SFSTGCHHEISAG 354

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RESULT 6
149341
MIP-1 alpha receptor like-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C:Accession: 149341
R:Gao, J.L.: Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokins
A:Reference number: 149339; MUID:95340546; PMID:7542241
A:Accession: 149341
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U28406; NID:g801551; PID:g801552
C:Superfamily: vertebrate rhodopsin

```

[illegible]

```

RESULT 7
G02436
chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CKR-3
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C:Accession: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272
A:Accession: G02436
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <PON>

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A:Cross-references: EMBL:U49127; NTD:g14775560; P1DN:AA09126.1; PID:g1477561
R:Combadere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor
A:Reference number: A57237; MUID:95348056; PMID:7622448
A:Accession: A57237
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <CON>
A:Cross-references: GB:U28654; NID:g1199579; P1DN:AAC50469.1; PID:g1199580
A:Note: the translated sequence in GenBank entry HS028694, release 113.0, P1DN:AAC504
C:Genetics:
A:Gene: GDB:CMKR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-119/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273, 106-183/Dissulfide bonds: #status predicted
F:34/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match	50.8%	Score 935.5	DB 2	Length 355
Best Local Similarity	53.0%	Pred. No. 5	6=70	
Matches	176	Conservative	63	Mismatches 90; Indels 3; Gaps 3
QY	20	CGKINVKQIAARLLPPLYSLVEIFGEVGNMLVILILINCKRUKSMIDLYLNLAIISDLFF	79	
DB	24	CEKADTRALMAQVFPPLXSLVETVGLIGLVNVAVYMLIKYRRLRIMTNVILNLAIISDLFF	83	
QY	80	LITVFFMAHYAAA-QMDFGNMCKQLTGLVIFGFSGIFFIILLTDRIYLVHAVFAAK	138	
DB	84	LVTLPFWHYHYGNHMMVFGHGCKRLISGFIHGLYSEIFFIILLTDRIYLVHAVFAAK	143	
QY	139	ARTVFEGVVTSITVTVVAVFAISLPGIIFRSCQEGILHYGSSHPYSOYQFNKNPQTKI	198	
DB	144	ARTVFEGVYITSVTVGLAVLALPFIETIETEELEBEYICSLYPIEDVIYSNRHFFTLAK	203	
QY	199	VILGVLPELVWVICYSGLIKTLTRCKRNEKKHRVRLIFTIMIVYELFWADYVNIYLLN	258	
DB	204	TIFGLVLPDLVWALICITGYTIKTLNCPSS-KKKYKAIKRLIFVYIMAVFIFWYTVYNAIILS	262	
QY	259	TFQEFEGGNANSSNRLLDAQOVYETTLGTHCCINPIYAYGKFRNTLVVFFQHIKAK	318	
DB	263	SYOSILIFENDCERTHLDLVMLVTEYIAVSHCCMPDVIAFYAFGERFRKYLRRHFHRLIM	322	
QY	319	RFCRCKSTFQCEAPERRASSVYRSGEQEISV	350	
DB	323	HLGRITPLPSEKERTSSV-SPSTAEPRLST	353	

RESULT 8
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A:Reference number: A57160; MUID:95370289; PMID:7642634
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POW>
A:Cross-references: GB:A5740; NID:g1370103; PIDN:CA59743.1; PID:g9771452
A:Note: source clone K5-5

C:Genetics:
 A:Gene: GDB:CKMBR4
 A:Cross-references: GDB:677463
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:281-308/Domain: transmembrane #status predicted <TM7>
 F:29-276,110-187/Disulfide bonds: #status predicted
 F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 49.9%; Score 919; DB 2; Length 360;

Best Local Similarity 49.9%; Pred. No. 1,3e-66;
 Matches 176; Conservative 66; Mismatches 99; Indels 10; Gaps 6;

OY 2 DYVSSPIYDINNTSE----PCKINVKQIAARLPPLYSLVIFGFGVGMVYLILIN 57
 DB 8 DTLDSEIYS-NYYLVESIPKPKCKEGIKAFGELFPLPSLVFVGLINSVVVLLFK 66
 OY 58 CKRLKMTDYLILNLAIISDLFELTVPFMAHYAAQDFGNTMQLTGLYFGFSGIF 117
 DB 67 YKRLRMTDYLILNLAIISDLFELTVPFMAHYAAQDFGNTMQLTGLYFGFSGIF 126
 OY 118 FIILITDRYLAHVAVFALKARTVTEGVTSVITVAVFASLPGLIFRSGREGHLYT 177
 DB 127 FVMLSIDRLATYHAFSLRARTLGVITSLATMSAVFASLPGLIFRSGREGHLYT 186
 OY 178 CSSIFPYSQYQFKNPTLIVILGLVPLVAVICSGIKTLIRNRNKKRAVRLI 237
 DB 187 CKRYSLINS-TTWKVLSSLEINILGLVPLIGIMLFCYSMIITLQHKNEKR-NKAVMI 244
 OY 238 FTIMIVFLFMAPYNIYLLNTFOEFGNLNCCSSNRDQAVTETLGMTHCCINPIY 297
 DB 245 FAVVVLFLGFWTPNINYLFLTELVELEVLDCTFERLDVAIQATETLAFVHCLNPIY 304
 OY 298 AFVGEKFRNTLVFQKHAKR--CKGCSIFQGEAPERASSVYTSSTGEDEI 348
 DB 305 FFLGEEKFRKTYILDLF-KTCRGLFVLCOYCGILDQIYSADTPSSSYTOSTMDHL 356

RESULT 9

JC4587

Chemokine (C-C) receptor 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C:Accession: JC4587

R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Blochem. Biophys. Res. Commun. 210, 337-343, 1996

A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A:Reference number: JC4587; MUID:96136324; PMID:8573157

A:Accession: JC4587

A:Molecule type: mRNA
 A:Residues: 1-360 <HOO>
 A:Cross-references: EMBL:X90863; NID:91167851; PIDN:CAA63372.1; PID:91167852

A:Experimental source: thymus

C:Genetics:
 A:Gene: cc ckr-4

C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus

F:72,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 49.2%; Score 906; DB 2; Length 360;

Best Local Similarity 49.9%; Pred. No. 1.6e-67;
 Matches 171; Conservative 69; Mismatches 97; Indels 6; Gaps 4;

OY 9 IYDINYY---TSEPCOKINVKQIAARLPPLYSLVIFGFGVGMVYLILINCKRLKMT 65
 DB 15 YVNSYIYESKPKCTKEGKAFGEVLPPLYSLVIFGLFGNSVVVLLFKIRLKSMT 74
 OY 66 DYLLNLAIISDLFELTVPFMAHYAAQDFGNTMQLTGLYFGFSGIFFIILITID 125
 DB 75 DYVLLNLAIISDLFELTVPFMAHYAAQDFGNTMQLTGLYFGFSGIFFIILITID 134
 OY 126 RYLAHVAVFALKARTVTEGVTSVITVAVFASLPGLIFRSGREGHLYTCSHPPYS 185
 DB 135 RYLAHVAVFALKARTVTEGVTSVITVAVFASLPGLIFRSGREGHLYTCSHPPYS 194
 OY 186 OYQFMRKQFTKTYILDLFGLVPLVAVICSGIKTLIRNRNKKRAVRLIPIYVFL 245
 DB 195 S-TTWKVLSSLEINILGLVPLIGIMLFCYSMIITLQHKNEKR-NKAVRIFGVVFL 252
 OY 246 LFMAPYNIYLLNTFOEFGNLNCCSSNRDQAVTETLGMTHCCINPIYAFGEKFR 305
 DB 253 GFVTPYVAVFLFTELVELEVLDCTFERLDVAIQATETLAFVHCLNPIYFLGKFR 312
 OY 306 NYLVFQKHAKR-FCKGCSIFQGEAPERASSVYTSSTGEDEI 347
 DB 313 KYIQLFRCTRGPLVLCCKHCDLQVYBADSSSYTOSTVDHD 355

RESULT 10

S55594

G protein-coupled receptor E1 - equine herpesvirus 2
 C:Species: equine herpesvirus 2
 C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C:Accession: S55594

R:Teiford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995

A:Title: The DNA sequence of equine herpesvirus 2.
 A:Reference number: S55594; MUID:95302501; PMID:7783207

A:Accession: S55594

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-383 <TEL>

A:Cross-references: GB:020824; NID:9695172; PIDN:AAC13788.1; PID:9695173

C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 45.0%; Score 829; DB 2; Length 383;
 Best Local Similarity 47.4%; Pred. No. 3.9e-61;
 Matches 157; Conservative 64; Mismatches 102; Indels 8; Gaps 3;

OY 11 DINYTSEPCOKINVKQIAARLPPLYSLVIFGFGVGMVYLILINCKRLKMTDYL 70
 DB 53 DYVDEEAPKCKSTTTLAAQVVALVFLFELGLGILNIVITVIRYMKKNTMMLL 112
 OY 71 NLAIISDLFELTVPFMAHYAAA--QWDFGNTMQLTGLYFGFSGIFFIILITID 128
 DB 113 NLAIISDLFELTVPFMAHYAAA--QWDFGNTMQLTGLYFGFSGIFFIILITID 172
 OY 129 AVYAVFALKARTVTEGVTSVITVAVFASLPGLIFRSGREGHLYTCSHPPYSO 188
 DB 173 AVYAVFALKARTVTEGVTSVITVAVFASLPGLIFRSGREGHLYTCSHPPYSO 232
 OY 189 FMRKQFTKTYILDLFGLVPLVAVICSGIKTLIRNRNKKRAVRLIPIYVFLFW 248
 DB 233 VMRRAHAKVIMLSLIPPLIMAVCYVITIRRLR-RPSKKRYAIRLIPYIAVYVFW 291
 OY 249 APYIVILLNTFOEFGNLNCCSSNRDQAVTETLGMTHCCINPIYAFGEKFRNYL 308
 DB 292 TPYIVILLNTFOEFGNLNCCSSNRDQAVTETLGMTHCCINPIYAFGEKFRNYL 351
 OY 309 LVFQKHAKR-FCKGCSIFQ-----GEAPER 334
 DB 352 YHFHYVAVLYLKYIPLPSGDEGKGPTR 382

RESULT 11

149340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: 149340
R:Geo: J.L. Murphy, P.M.
J. Biol. Chem. 270, 1794-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
A:Reference number: 149339; MUID:95340546; PMID:7542241
A:Accession: 149340
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-356 <RES>
A:Cross-references: EMBL:U28405; NID:9881549; PIDN:AAA89154.1; PID:9881550
C:Superfamily: vertebrate rhodopsin

Query Match 43.4%; Score 799.5; DB 2; Length 356;
Best Local Similarity 45.0%; Pred. No. 9,9e-59;
Matches 159; Conservative 68; Mismatches 119; Indels 7; Gaps 4;

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OY 5 VSSPIYDI---NYTSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKR 60
DB 6 VTEPSYNTFAKNDPMSGFLCFESINVRAGITVPTLSLVIFIGVIGHVAVLVLIQHR 65
OY 61 LKSMIDYILNLAISDLFEFLTPVPMANH-AAQWDFGNTGQLLGLYFEGFSGIFPT 119
DB 66 LKNMTSYLFLNLAISDLFEFLTPVPMANH-AAQWDFGNTGQLLGLYFEGFSGIFPT 125
OY 120 ILTIDRYLAVVAHFAFKARTVGVVSVITWVAFAFLPGIIFRSQEGHLYTCS 179
DB 126 TLTIDRYLAVVAHFAFKARTVGVVSVITWVAFAFLPGIIFRSQEGHLYTCS 185
OY 180 SHEPPSYQVQFKNFQTLKIVILGLVPLVAVICSGILKTLRCRNEKKRRRAVLTPT 239
DB 186 ALTPKSLIRFLRFQALTNMILGLIPLAMTICVRIINVLHR-RPNKKKAKVMKLTPV 244
OY 240 IIVYFLFMAPIYVLLNTFOEFGLNCCSSNNRLDAQOAYETELGTHCCINPIYAF 299
DB 245 ILLFPLLPARYIAFAFADVDLETPSCLSQOVDLSMTTEALAYHCCVNPVITYAF 304
OY 300 VGEKFRNYLVLFQKHIAKRFCKCSIFQOAPERRASSYTRSTGEQIEISVGL 352
DB 305 VGRKFRKYLMOFLRRHTAITLPLQMLFLESDRAQRASA-RLPSTVEIETRSADL 356

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RESULT 12

JC5067
G protein-coupled receptor CKR-11 - human
N:Alternate names: chemokine receptor-like protein TER1; GPR-CX6
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JCS067; G02776; G02387
R:Abdellos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
A:Reference number: JCS067; MUID:97040707; PMID:8886020
A:Accession: JCS067
A:Molecule type: DNA
A:Residues: 1-355 <TAB>
A:Cross-references: EMBL:279782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736
R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: H01714
A:Accession: G02776
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <NAP>
A:Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R:Bonner, T.I.
submitted to the EMBL Data Library, January 1996

A:Reference number: H01154

A:Accession: G02387
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <BON>
A:Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C:Comment: This protein belongs to the family of beta chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR8; CMKBR2L; TER1; CKR-11
A:Cross-references: GDB:6053733; OMIM:601834
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:36-63/Domain: transmembrane #status predicted <TM1>
F:73-94/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-177/Domain: transmembrane #status predicted <TM4>
F:200-222/Domain: transmembrane #status predicted <TM5>
F:239-260/Domain: transmembrane #status predicted <TM6>
F:281-304/Domain: transmembrane #status predicted <TM7>

Query Match 40.5%; Score 746.5; DB 2; Length 355;
Best Local Similarity 41.1%; Pred. No. 2,4e-54;
Matches 148; Conservative 66; Mismatches 125; Indels 21; Gaps 6;

```

OY 1 MDYQVSSPIYDI-NY-----TSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVIL 55
DB 1 MDYTLDSVTYVTDYDYDFDFSSPCDAELIQNGKILLAVFCILFESLLGNSLVILVL 60
OY 56 INCKRLKSMFDYILNLAISDLFEFLTPVPMANH-AAQWDFGNTGQLLGLYFEGFSG 115
DB 61 VVCKRLKSTTDYILNLAISDLFEFLTPVPMANH-AAQWDFGNTGQLLGLYFEGFSG 120
OY 116 IFFIILTDRLAVVAHFAFKARTVGVVSVITWVAFAFLPGIIFRSQEGHLYTCS 175
DB 121 MFFITLMSDRYLAVVAHFAFKARTVGVVSVITWVAFAFLPGIIFRSQEGHLYTCS 180
OY 176 YVCSHPPSYQVQFKNFQTLKIVILGLVPLVAVICSGILKTLRCRNEKKRRRAVLTPT 239
DB 181 LQCYG-FYNOQTLKAKRIFNFQNTLIGLIPETIMFCYIKLHLKRCQNNKT-KAIR 238
OY 236 LLETTIYVFLFMAPIYVLLNTFOEFGLNCCSSNNRLDAQOAYETELGTHCCINPIYAF 299
DB 239 LVLIYVIAFLFVFPVNVVLTSLSHMIIIDCGISQGLYATVETIISTHCCVNPV 298
OY 296 IYAFVGEKFRNYLVLFQKHIAKRFCKCSIFQOAPERRASSYTRSTGEQIEISVGL 348
DB 299 IYAFVGEKFRKHLSEIFQK-----SCSQIFNYILGRQMPRESCKSSSCQOHSRSSSV 351

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RESULT 13

I58186
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I58186
R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord an
A:Reference number: I58186; MUID:94323113; PMID:8047298
A:Accession: I58186
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U04808; NID:g2558635; PIDN:AA87093.1; PID:g439861
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 38.7%; Score 712; DB 2; Length 354;
Best Local Similarity 40.6%; Pred. No. 1,7e-51;
Matches 147; Conservative 59; Mismatches 126; Indels 30; Gaps 6;

OY 6 SPSPIYDINY-----TSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKRL 61

```

Db      4 SPPELDLENFEDSDSACVYLGDIYVAGFTFLSIFSLVFTFGVGNLVLAITNSRKS 63
Oy      62 KSMTDIYLLNLAISDLPFLTPFMAHYAAQWDFNTMCOLLTLGLTFGFSIGFTIL 121
        64 KSTIDYLLNLAISDLPFLTPFMAHYAAQWDFNTMCOLLTLGLTFGFSIGFTIL 123
Oy      122 LTRDYLAIVLAHVAFAKARFTGVTVSVITWVAVFASLPGLIIFTRSQEGLYTSSH 181
        124 ISIDRYLAIVLAHVAFAKARFTGVTVSVITWVAVFASLPGLIIFTRSQEGLYTSSH 179
Oy      182 FFSQVQFMKNFQTLKVIIGVPLIYVYICSGILTKLRCNEKRRAVRLFTIM 241
        180 YPEVLDIWPVLRSEVNIIGFVLPILIMSCFYRIYRTFSCNKRKA-RAIRLLLV 238.
Oy      242 IYVFLFAPYNIYVLLTFQEFGLNCSNNRLDAQOVETLGMTKCCINPIYAFV 301
        239 VVEFLFPTNYIYVLETLKFYNFPCGKRLRLALSTERYAFSHCLNPIYAFV 298
Oy      302 EKFRNVLVFPQKHIAKRCSCIF-----QGEAPERASSVYTRSTGEQEI 348
        299 EKFRNVLVFPQKHIAKRCSCIF-----QGEAPERASSVYTRSTGEQEI 350
Oy      349 SV 350
        351 SL 352

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RESULT 14

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JC5942
Chemokine receptor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JC5942
R:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A:Title: Cloning and characterization of a novel human chemokine receptor.
A:Reference number: JC5942; MUID:98139902; PMID:9473515
A:Accession: JC5942
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-344 <FAN>
A:Cross-references: GB:097123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
C:Superfamily: vertebrate rhodopsin

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Query Match      36.6%; Score 673; DB 2; Length 344;
Best Local Similarity 40.9%; Pred. No. 2,86-48;
Matches 137; Conservative 64; Mismatches 108; Indels 26; Gaps 7;

Oy      17 SEPCQKINVKQIARLLPPLYSLVIFGFGNMLVILLNCRKLRKSMTDIYLLNLAISD 76
        25 AEQCDKDAQALSAQLPPLCSAVFVIGVLDNLLVILVYKGLKRENIYLLNLAISN 84
Oy      77 LFFLLTPFMAHYAAQWDFNTMCOLLTLGLTFGFSIGFTILTRDYLAIVH-AYF 135
        85 LCFLLTPFMAHYAAQWDFNTMCOLLTLGLTFGFSIGFTILTRDYLAIVH-AYF 138
Oy      136 ALKARTVPGVTVSVITWVAVFASLPGLIIFTRSQEGLYTSS-SHEPY--SOYQFMKN 192
        139 FSARRRRPGCITISVLAHVAFAKARFTGVTVSVITWVAVFASLPGLIIFTRSQEGLYTSS 198
Oy      193 FQTLKMNISVLPFLFTFLYQMRKTL--RREQRYSLEKLVAFALMVFLMMAAPYN 255
        199 FQTLKMNISVLPFLFTFLYQMRKTL--RREQRYSLEKLVAFALMVFLMMAAPYN 252
Oy      253 IYVLLNTPFQEFGLNCSNNRLDAQOVETLGMTKCCINPIYAFGEKFRNVLVFPQKH 312
        256 IAFPLSTFKHFHSIDKSSYNLDSVHTKLLATFTCCINPLLAFLDGTESKYL---- 311
Oy      313 QKHIAKRCSCIFQGEAPERASSVYTRSTGEQEI 347
        312 -----CRCPIL-RSNTPLQPRGSAQGTSTREE 337

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RESULT 15

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JC4304
orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C:Species: Homo sapiens (man)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C:Accession: JC4304
R:Report, C.J.; Schwickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to
A:Reference number: JC4304; MUID:96011651; PMID:7590284
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U20350; NID:g665580; PIDN:AAA1783.1; PID:g665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signals
C:Genetics:
A:Gene: v28
A:Map position: 3pter-p21
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>

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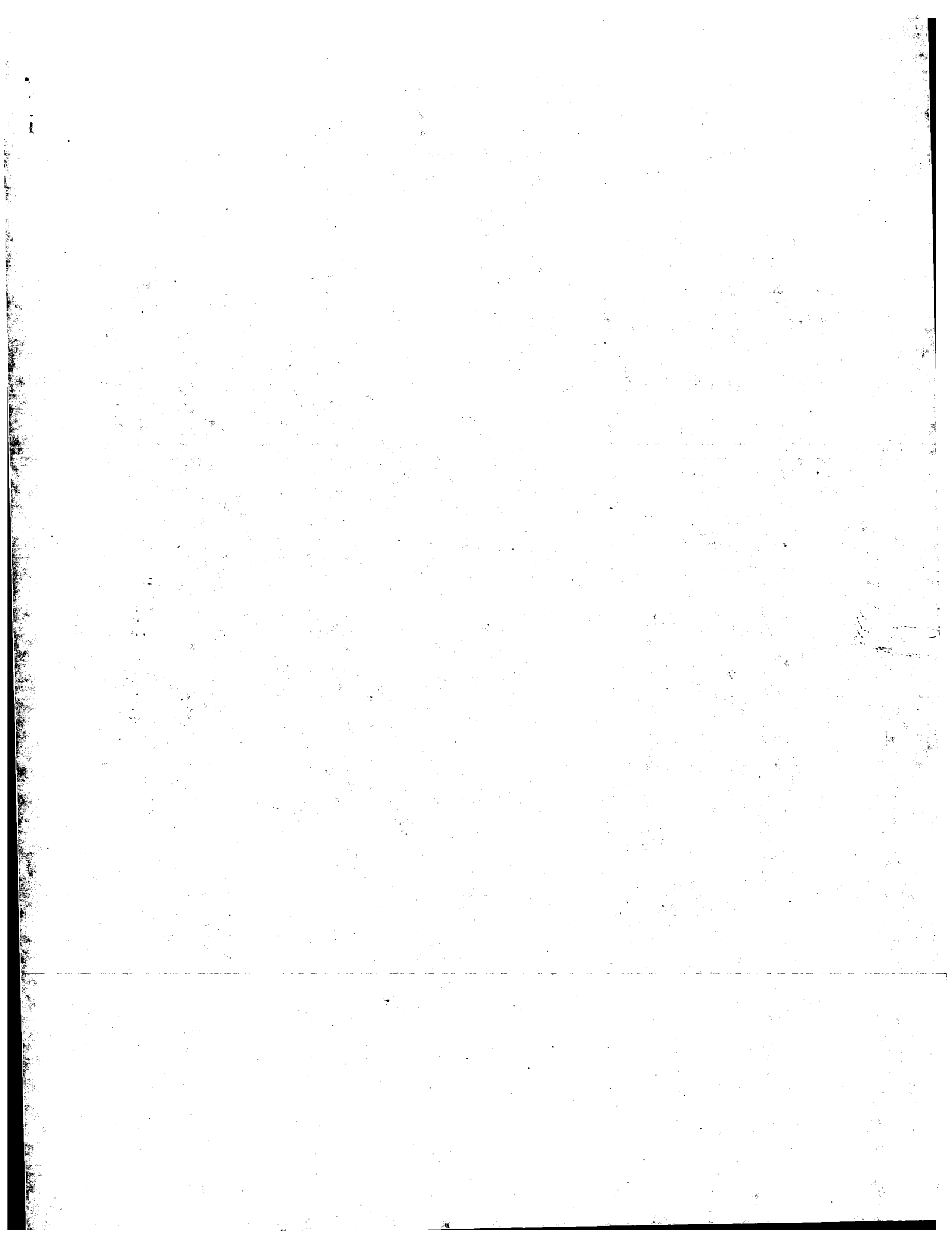
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Query Match      36.4%; Score 670.5; DB 2; Length 355;
Best Local Similarity 42.9%; Pred. No. 4,66-48;
Matches 129; Conservative 55; Mismatches 112; Indels 5; Gaps 3;

Oy      17 SEPCQKINVKQIARLLPPLYSLVIFGFGNMLVILLNCRKLRKSMTDIYLLNLAISD 76
        18 AEACYIDIVFQVFLSIFYSYFAIGLVGNLLVFPALNRSKRPSTVDIYLLNLAISD 77
Oy      77 LFFLLTPFMAHYAAQWDFNTMCOLLTLGLTFGFSIGFTILTRDYLAIVH-AYF 136
        78 LFFLLTPFMAHYAAQWDFNTMCOLLTLGLTFGFSIGFTILTRDYLAIVH-AYF 137
Oy      137 LKARTVPGVTVSVITWVAVFASLPGLIIFTRSQEGLYTSS-SHEPY--SOYQFMKNFQTL 196
        138 MNRTVGHGVTISGVAAAILVAAPQFMFK-QKEN---ECLGDYEVLDIYVLAIRNV 193
Oy      197 KIYVLGLVPLVAVICYSGLTKTLRCNEKRRAVRLFTIMYVFLFMAPIYVLL 256
        194 ETNPLGFLPLLLIMSYCFRIQTLFSCNKRKA-KAIIKLLVAVIVFPLFPMYVIMIF 252
Oy      257 LNTFQEFGLNCSNNRLDAQOVETLGMTKCCINPIYAFGEKFRNVLVFPQKH 316
        253 LETKLYDFPSCDMRDLRLALSTERYAFSHCLNPLIYAFGEKFRNVLVFPQKH 312
Oy      317 A 317
        313 A 313

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Search completed: June 3, 2003, 15:22:40
Job time : 34.2822 secs



[6] SEQUENCE FROM N.A., AND POLYMORPHISMS.
 MEDLINE-98022612; Pubmed-9359654;
 Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 Ho D.L.,
 RA HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 [7]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-98049523; Pubmed-9388201.
 RX Munnidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RA "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for
 RL polymorphisms within the regulatory regions and noncoding exons".
 J. Biol. Chem. 272:30662-30671(1997).
 [8]
 RN SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RP Magderowaska M., Barre-Sinoussi F., Issatiras H., Theodorou I.,
 RA Degre P.;
 RL submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 [9]
 RN CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RP MEDLINE-96260017; Pubmed-8649511.
 RX Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 RT Pelger S.C., Schall T.J., Littman D.R., Landau N.R.;
 RL "Identification of a major co-receptor for primary isolates of
 HIV-1".
 Nature 381:661-666(1996).
 [10]
 RN CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RP MEDLINE-96260018; Pubmed-8649512;
 RX Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RL CC-CKR-5".
 Nature 381:667-673(1996).
 [11]
 RN SULFATION.
 RP MEDLINE-99189752; Pubmed-10089882;
 RX Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 entry".
 Cell 96:667-676(1999).
 [12]
 RN FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
 CC SYNCYTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
 CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
 CC -1- PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
 CC -1- PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
 CC GLYCOSYLATION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; X91492; CAA62798.1; -
 DR EMBL; U54994; AAC50598.1; -
 DR EMBL; U57840; AB017071.1; -
 DR EMBL; U93626; AB057193.1; -
 DR EMBL; U83326; AAC51797.1; -

DR	EMBL	AF011500;	AAB65700.1; -
DR	EMBL	AF011501;	AAB65701.1; -
DR	EMBL	AF011502;	AAB65702.1; -
DR	EMBL	AF011503;	AAB65703.1; -
DR	EMBL	AF011505;	AAB65705.1; -
DR	EMBL	AF011506;	AAB65706.1; -
DR	EMBL	AF011507;	AAB65707.1; -
DR	EMBL	AF011508;	AAB65708.1; -
DR	EMBL	AF011509;	AAB65709.1; -
DR	EMBL	AF011510;	AAB65710.1; -
DR	EMBL	AF011511;	AAB65711.1; -
DR	EMBL	AF011512;	AAB65712.1; -
DR	EMBL	AF011513;	AAB65713.1; -
DR	EMBL	AF011514;	AAB65714.1; -
DR	EMBL	AF011515;	AAB65715.1; -
DR	EMBL	AF011516;	AAB65716.1; -
DR	EMBL	AF011517;	AAB65717.1; -
DR	EMBL	AF011518;	AAB65718.1; -
DR	EMBL	AF011519;	AAB65719.1; -
DR	EMBL	AF011520;	AAB65720.1; -
DR	EMBL	AF011521;	AAB65721.1; -
DR	EMBL	AF011522;	AAB65722.1; -
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DR	EMBL	AF011526;	AAB65726.1; -
DR	EMBL	AF011527;	AAB65727.1; -
DR	EMBL	AF011528;	AAB65728.1; -
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DR	EMBL	AF011532;	AAB65732.1; -
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DR	EMBL	AF011536;	AAB65736.1; -
DR	EMBL	AF011537;	AAB65737.1; -
DR	EMBL	AF031237;	AAB94735.1; -
DR	GeneW;	HGNC:1606;	CCRS.
DR	MIM;	601373;	-
DR	InterPro;	IPR000276;	GPCR_Rhodpsn.
DR	Pfam;	PF00001;	7tm.1; 1.
DR	PRINTS;	PR000237;	GPCRHODOPSN.
DR	PROSITE;	PS00237;	G.PROTEIN_RECPT_P1_1.
DR	PROSITE;	PS00264;	G.PROTEIN_RECPT_P2_1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein		
KW	Polyomorphism.		
KM	DOMAIN	1	30
FT	TRANSMEM	31	58
FT	DOMAIN	59	68
FT	TRANSMEM	69	89
FT	DOMAIN	90	102
FT	TRANSMEM	103	124
FT	DOMAIN	125	141
FT	TRANSMEM	142	166
FT	DOMAIN	167	198
FT	TRANSMEM	199	218
FT	DOMAIN	219	235
FT	TRANSMEM	236	260
FT	DOMAIN	261	277
FT	TRANSMEM	278	301
FT	DOMAIN	302	352
FT	DISULFID	101	178
FT	MOD_RES	3	3
FT	MOD_RES	10	10
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Query Match 100.0%; Score 1841; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 9, 6e-92;
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OY 1 MDYVSSPIYDINTYSEPOKINVKQIAARLPPLSLVFIFGFGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINTYSEPOKINVKQIAARLPPLSLVFIFGFGNMLVILLINCKR 60
 OY 61 LKSWTDIYLLNLAISDLFFLLTVPFMAHYAAQDFGNTMQLLTGLYPTGFSGIFPII 120
 DB 61 LKSWTDIYLLNLAISDLFFLLTVPFMAHYAAQDFGNTMQLLTGLYPTGFSGIFPII 120
 OY 121 LRTDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFRSQEGSLHYTCS 180
 DB 121 LRTDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFRSQEGSLHYTCS 180
 OY 181 HFPYSOYQFKNKNOTLKIYVLGLVPLLVNVCISGLTKTLRCRNKKRRAVRLFTI 240
 DB 181 HFPYSOYQFKNKNOTLKIYVLGLVPLLVNVCISGLTKTLRCRNKKRRAVRLFTI 240
 OY 241 MIYVFLFMAPIYNIYLLNTEQFGLNCCSSNRLDQAMQVETLGMTGCCINPIIYAFV 300
 DB 241 MIYVFLFMAPIYNIYLLNTEQFGLNCCSSNRLDQAMQVETLGMTGCCINPIIYAFV 300
 OY 301 GEFERNYLLVFFQNHAKRCKCCSIFQEAPEBASVYTRSTGEQISVGL 352
 DB 301 GEFERNYLLVFFQNHAKRCKCCSIFQEAPEBASVYTRSTGEQISVGL 352

RESULT 2
 CKR5_PANTR STANDARD; PRT; 352 AA.
 ID CKR5_PANTR STANDARD; PRT; 352 AA.
 AC P56440; 002778;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 NC NCBI_TaxID:9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97268687; Pubmed-9108095;
 RA Edinger A.L., Amodeo A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Balper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98022612; Pubmed-9359654;
 RA Zhang L., Caruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97426118; Pubmed-9282822;
 RA Zacharova V., Zachar V., Goulet A.S.;
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 RT HIV type 1 host.";
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98090115; Pubmed-9430250;

RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@ebi.ac.uk).

DR EMBL: AF005663; AAB62557.1; -
 DR EMBL: U94329; AAB58446.1; -
 DR EMBL: AF011542; AAB65742.1; -
 DR EMBL: U97666; AAC51670.1; -
 DR EMBL: AF011540; AAB65740.1; -
 DR EMBL: U89797; AAC03717.1; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECP_F1_2; 1.
 DR KMW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 123 123
 FT SEQUENCE 352 AA; 40539 MW; 4A33E98B80FE34C CRC64;

Query Match 99.7%; Score 1835; DB 1; Length 352;
 Best Local Similarity 99.4%; Pred. No. 2e-91;
 Matches 350; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYVSSPIYDINTYSEPOKINVKQIAARLPPLSLVFIFGFGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINTYSEPOKINVKQIAARLPPLSLVFIFGFGNMLVILLINCKR 60
 OY 61 LKSWTDIYLLNLAISDLFFLLTVPFMAHYAAQDFGNTMQLLTGLYPTGFSGIFPII 120
 DB 61 LKSWTDIYLLNLAISDLFFLLTVPFMAHYAAQDFGNTMQLLTGLYPTGFSGIFPII 120
 OY 121 LRTDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFRSQEGSLHYTCS 180
 DB 121 LRTDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFRSQEGSLHYTCS 180
 OY 181 HFPYSOYQFKNKNOTLKIYVLGLVPLLVNVCISGLTKTLRCRNKKRRAVRLFTI 240

Db 181 HEPYSOYQFMKNFQTLKIVILGLVPLLMVICYSGILKTLRCRNEKRRRAVRLIFTI 240

QY 241 MIVYFLFAPRYNIVLLMTFOEFGILNCCSSNRDQAMQVETLGMTHCCINPIYAFV 300

Db 241 MIVYFLFAPRYNIVLLMTFOEFGILNCCSSNRDQAMQVETLGMTHCCINPIYAFV 300

QY 301 GEFKNYLLVFFQKHIAKFCCKCSIFQOEAPERASSYVTRSTGEOISVGL 352

Db 301 GEFKNYLLVFFQKHIAKFCCKCSIFQOEAPERASSYVTRSTGEOISVGL 352

RESULT 3

CCR5_PONPY STANDARD: PRT: 352 AA.

AC 097881:

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).

GN CCR5 OR CCKBR5.

OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.

OX NCBI_TaxID=9600;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99416438; PubMed=10486970;

RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.

RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."

RL Mol. Biol. Evol. 16:1145-1154(1999).

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AF075446; AAD19858.1; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR_Rhodopsn.

DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.

DR PROSITE: PS00262; G-PROTEIN_RECPT_F1_2; 1.

GN G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30

FT TRANSMEM 1 58

FT DOMAIN 59 68

FT TRANSMEM 69 89

FT DOMAIN 90 102

FT TRANSMEM 103 124

FT DOMAIN 125 141

FT TRANSMEM 142 166

FT DOMAIN 167 198

FT TRANSMEM 199 218

FT DOMAIN 219 235

FT TRANSMEM 236 260

FT DOMAIN 261 277

FT TRANSMEM 278 301

FT DOMAIN 302 352

FT DISULFID 101 178

FT MOD_RES 3 3

FT MOD_RES 10 10

FT MOD_RES 14 14

FT MOD_RES 15 15

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 99.4%; Score 1830; DB 1; Length 352;

Best Local Similarity 99.1%; Pred. No. 3.7e-91;

Matches 349; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINVTYSPCKINVKQIAARLLPLYSIVTFGFGNMLVILLINCKR 60

Db 1 MDYVSSPIYDIDYTSPECOKINVKQIAARLLPLYSIVTFGFGNMLVILLINCKR 60

QY 61 LKSMIDYILNLAISDLEFLLTVPMAYAAQWFGMTQQLTGLTFIFGFSIGFTI 120

Db 61 LKSMIDYILNLAISDLEFLLTVPMAYAAQWFGMTQQLTGLTFIFGFSIGFTI 120

QY 121 LITDRYLAIVAAVPAALAKRYTEGVYVSVITWVAVASLPGIIFTRSOEGLYTCS 180

Db 121 LITDRYLAIVAAVPAALAKRYTEGVYVSVITWVAVASLPGIIFTRSOEGLYTCS 180

QY 181 HEPYSOYQFMKNFQTLKIVILGLVPLLMVICYSGILKTLRCRNEKRRRAVRLIFTI 240

Db 181 HEPYSOYQFMKNFQTLKIVILGLVPLLMVICYSGILKTLRCRNEKRRRAVRLIFTI 240

QY 241 MIVYFLFAPRYNIVLLMTFOEFGILNCCSSNRDQAMQVETLGMTHCCINPIYAFV 300

Db 241 MIVYFLFAPRYNIVLLMTFOEFGILNCCSSNRDQAMQVETLGMTHCCINPIYAFV 300

QY 301 GEFKNYLLVFFQKHIAKFCCKCSIFQOEAPERASSYVTRSTGEOISVGL 352

Db 301 GEFKNYLLVFFQKHIAKFCCKCSIFQOEAPERASSYVTRSTGEOISVGL 352

RESULT 4

CCR5_GORGO STANDARD: PRT: 352 AA.

AC P56439;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).

GN CCR5 OR CCKBR5.

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.

OX NCBI_TaxID=9595;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97268687; PubMed=9108095;

RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharpton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M., Pelper S.C., Farnettler M., Broder C.C., Doms R.W.

RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."

RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AF006559; AAB62553.1; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR_Rhodopsn.

DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1: 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2: 1.
 RM G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSSEM 31 58
 FT TRANSSEM 59 68
 FT TRANSSEM 69 88
 FT TRANSSEM 90 102
 FT TRANSSEM 103 124
 FT TRANSSEM 125 141
 FT TRANSSEM 142 166
 FT TRANSSEM 167 198
 FT TRANSSEM 199 218
 FT TRANSSEM 219 235
 FT TRANSSEM 236 260
 FT TRANSSEM 261 277
 FT TRANSSEM 278 301
 FT TRANSSEM 302 352
 FT DISUFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 SO SEQUENCE 352 AA; 40515 MW; D06FCB9F5EAC64 CRC64;

Query Match 99.1%; Score 1825; DB 1; Length 352;
 Best Local Similarity 98.9%; Pred. No. 6.8e-91;
 Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDYVSSPIVDIYNTSEPCOKINVKQIARLLPPLSLVFIKFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIVDIYNTSEPCOKINVKQIARLLPPLSLVFIKFGVGNMLVILLINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLVPEFMAHYAAQMDFGNTMQLLTGLYFIKFGSGIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLVPEFMAHYAAQMDFGNTMQLLTGLYFIKFGSGIFPII 120
 QY 121 LITIDRYLAVVHAFAKARTVPGVTVSYTVVAVFASLPGLIIFRSOKEGLHYTCSS 180
 DB 121 LITIDRYLAVVHAFAKARTVPGVTVSYTVVAVFASLPGLIIFRSOKEGLHYTCSS 180
 QY 181 HEPYSOYQFKNFOTLKIIVILGLVPLVWVICSGILTKTLRCRNRKRRHRAVRLFTI 240
 DB 181 HEPYSOYQFKNFOTLKIIVILGLVPLVWVICSGILTKTLRCRNRKRRHRAVRLFTI 240
 QY 241 MIYVFLFWAPYNIYLLNTFOEFGGLNCCSSNRLDQAMOVETLTGTHCCINPIIYAFV 300
 DB 241 MIYVFLFWAPYNIYLLNTFOEFGGLNCCSSNRLDQAMOVETLTGTHCCINPIIYAFV 300
 QY 301 GEKFRNTLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 DB 301 GEKFRNTLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 5
 CKR5_TRAPH STANDARD; PRT; 352 AA.
 AC 097879;
 DT 30-MAY-2000 (Rel. 39, Last Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C Chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CKR5.
 OS Trachypithecus phayrei (Phayre's leaf monkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus.
 OX NCBI_Taxid=61616;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";

RL MOL. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@1ab.gib.ch).
 DR EMBL: AF075443; AAD19655.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR000237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1: 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2: 1.
 RM G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSSEM 31 58
 FT TRANSSEM 59 68
 FT TRANSSEM 69 88
 FT TRANSSEM 90 102
 FT TRANSSEM 103 124
 FT TRANSSEM 125 141
 FT TRANSSEM 142 166
 FT TRANSSEM 167 198
 FT TRANSSEM 199 218
 FT TRANSSEM 219 235
 FT TRANSSEM 236 260
 FT TRANSSEM 261 277
 FT TRANSSEM 278 301
 FT TRANSSEM 302 352
 FT DISUFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 SO SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 98.9%; Score 1821; DB 1; Length 352;
 Best Local Similarity 98.0%; Pred. No. 1.1e-90;
 Matches 345; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPIVDIYNTSEPCOKINVKQIARLLPPLSLVFIKFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIVDIYNTSEPCOKINVKQIARLLPPLSLVFIKFGVGNMLVILLINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLVPEFMAHYAAQMDFGNTMQLLTGLYFIKFGSGIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLVPEFMAHYAAQMDFGNTMQLLTGLYFIKFGSGIFPII 120
 QY 121 LITIDRYLAVVHAFAKARTVPGVTVSYTVVAVFASLPGLIIFRSOKEGLHYTCSS 180
 DB 121 LITIDRYLAVVHAFAKARTVPGVTVSYTVVAVFASLPGLIIFRSOKEGLHYTCSS 180
 QY 181 HEPYSOYQFKNFOTLKIIVILGLVPLVWVICSGILTKTLRCRNRKRRHRAVRLFTI 240
 DB 181 HEPYSOYQFKNFOTLKIIVILGLVPLVWVICSGILTKTLRCRNRKRRHRAVRLFTI 240
 QY 241 MIYVFLFWAPYNIYLLNTFOEFGGLNCCSSNRLDQAMOVETLTGTHCCINPIIYAFV 300
 DB 241 MIYVFLFWAPYNIYLLNTFOEFGGLNCCSSNRLDQAMOVETLTGTHCCINPIIYAFV 300
 QY 301 GEKFRNTLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
 DB 301 GEKFRNTLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 6
 CCR5_PAPHA STANDARD: PRT: 352 AA.
 ID CCR5_PAPHA
 AC P56441;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecidae; Papio.
 OX NCBI_TaxID=9557, 9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-P. hamadryas;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peliper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC SPECIES-P. hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Sakena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lai R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RT nonhuman primates.";
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-P. anubis;
 RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: AF005658; AAB62552.1; -;
 DR EMBL: AF105287; AAD20556.1; -;
 DR EMBL: AF105288; AAD20557.1; -;
 DR EMBL: AF105289; AAD20558.1; -;
 DR EMBL: AF105290; AAD20559.1; -;
 DR EMBL: AF023452; AAC63830.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1;
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1.1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1
 FT TRANSMEM 31 58
 FT DOMAIN 1 (POTENTIAL).
 FT TRANSMEM 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 2 (POTENTIAL).
 FT DOMAIN 90 102
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 FT CARBOHYD 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9B1FE8B2 CRC64;
 Query Match 98.6%; Score 1816; DB 1; Length 352;
 Best Local Similarity 98.0%; Pred. No. 2,1e-90;
 Matches 345; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDYVSSPIYDINNTYTSPECQKINVKQIAARLLPLYSIVTEFGVGMVLLILNKR 60
 DB 1 MDYVSSPIYDIDYTSPECQKINVKQIAARLLPLYSIVTEFGVGMVLLILNKR 60
 QY 61 LKSMIDYLLNLAISDLFFLLVPPMAHYAAQWDFGNTMQLTGLYFIFGFSGIFPII 120
 DB 61 LKSMIDYLLNLAISDLFFLLVPPMAHYAAQWDFGNTMQLTGLYFIFGFSGIFPII 120
 QY 121 LITDRIYLAHVAAALKARYTREVYVSVITWVAVASLPGLIFTSQKGLHYTSS 180
 DB 121 LITDRIYLAHVAAALKARYTREVYVSVITWVAVASLPGLIFTSQKGLHYTSS 180
 QY 121 LITDRIYLAHVAAALKARYTREVYVSVITWVAVASLPGLIFTSQKGLHYTSS 180
 DB 121 LITDRIYLAHVAAALKARYTREVYVSVITWVAVASLPGLIFTSQKGLHYTSS 180
 QY 181 HPPYSOYOFMKKFOFLKIYIIGLVPLLMVTCISGILKTLRCNEKKRHHAVLIPTI 240
 DB 181 HPPYSOYOFMKKFOFLKIYIIGLVPLLMVTCISGILKTLRCNEKKRHHAVLIPTI 240
 QY 181 HPPYSOYOFMKKFOFLKIYIIGLVPLLMVTCISGILKTLRCNEKKRHHAVLIPTI 240
 DB 181 HPPYSOYOFMKKFOFLKIYIIGLVPLLMVTCISGILKTLRCNEKKRHHAVLIPTI 240
 QY 241 MIVYELFMAPIYVILLNTFOEFFGLNNCSSNRDQAMQVETLGMTHCCINPIYAFV 300
 DB 241 MIVYELFMAPIYVILLNTFOEFFGLNNCSSNRDQAMQVETLGMTHCCINPIYAFV 300
 QY 301 GEFKNYLLVFPQKHIAKFCSCSIPOEAEERASVYTRSTGOEISVGL 352
 DB 301 GEFKNYLLVFPQKHIAKFCSCSIPOEAEERASVYTRSTGOEISVGL 352
 DB 301 GEFKNYLLVFPQKHIAKFCSCSIPOEAEERASVYTRSTGOEISVGL 352
 DB 301 GEFKNYLLVFPQKHIAKFCSCSIPOEAEERASVYTRSTGOEISVGL 352
 RESULT 7
 CCR5_TRAFR STANDARD: PRT: 352 AA.
 ID CCR5_TRAFR
 AC Q97878;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5).
 GN CCR5 OR CCR5.
 OS Trachypithecus francoisi (Francoisi 'langur' (Indochinese langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus.
 OX NCBI_TaxID=54180;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RT Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL: AF075442; AAD19854.1;
 DR Interpro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1;
 DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein; sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 SQ SEQUENCE 352 AA; 40496 MW; 4366F148C25538F CRC64;
 Query Match 98.6%; Score 1816; DB 1; Length 352;
 Best Local Similarity 97.7%; Pred. No. 2.1e-90;
 Matches 344; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDYVSSPIYDINVTYSEPCQKINVOIARLLPLYSLVIFGVGNMVLILNCKR 60
 DB 1 MDYVSSPIYDINVTYSEPCQKINVOIARLLPLYSLVIFGVGNMVLILNCKR 60
 QY 61 LKSMTDIYLLNLALISDLFFLLVTFPFAHYAAQMDGNTMCOGLTGLYFIFGFSGIFETI 120
 DB 61 LKSMTDIYLLNLALISDLFFLLVTFPFAHYAAQMDGNTMCOGLTGLYFIFGFSGIFETI 120
 QY 121 LITIDRYLAVVAVFALKARTVTGVTSVITVVAVFASLPGIIFTRSOKEGLHYTCS 180
 DB 121 LITIDRYLAVVAVFALKARTVTGVTSVITVVAVFASLPGIIFTRSOKEGLHYTCS 180
 QY 122 LITIDRYLAVVAVFALKARTVTGVTSVITVVAVFASLPGIIFTRSOKEGLHYTCS 180
 DB 122 LITIDRYLAVVAVFALKARTVTGVTSVITVVAVFASLPGIIFTRSOKEGLHYTCS 180
 QY 181 HEPYSOYQFQKMFQTLKIVILGLVPLVAVICSGILKTLTLCRNEKKRRAVRILFTI 240
 DB 181 HEPYSOYQFQKMFQTLKIVILGLVPLVAVICSGILKTLTLCRNEKKRRAVRILFTI 240
 QY 241 MIVYELFMAPYNYVILLNTPQEFPGINSSNRLOAOQVETLGMTNHCINPIITAFV 300
 DB 241 MIVYELFMAPYNYVILLNTPQEFPGINSSNRLOAOQVETLGMTNHCINPIITAFV 300
 QY 301 GEFKRYLLVFQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQIEVGL 352
 DB 301 GEFKRYLLVFQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQIEVGL 352
 DB 301 GEFKRYLLVFQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQIEVGL 352
 RESULT 8
 CKRS_PYGBI STANDARD; PRT; 352 AA.
 ID CKRS_PYGBI
 AC 097880;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 GN C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CKRS).
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinothecus bieti).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 NCBI_TaxID=61621;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKRS chemokine receptor gene in primates";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL: AF075445; AAD19857.1;
 DR Interpro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1;
 DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein; sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;
 Query Match 98.6%; Score 1815; DB 1; Length 352;
 Best Local Similarity 97.7%; Pred. No. 2.3e-90;
 Matches 344; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDYVSSPIYDINVTYSEPCQKINVOIARLLPLYSLVIFGVGNMVLILNCKR 60
 DB 1 MDYVSSPIYDINVTYSEPCQKINVOIARLLPLYSLVIFGVGNMVLILNCKR 60
 QY 61 LKSMTDIYLLNLALISDLFFLLVTFPFAHYAAQMDGNTMCOGLTGLYFIFGFSGIFETI 120
 DB 61 LKSMTDIYLLNLALISDLFFLLVTFPFAHYAAQMDGNTMCOGLTGLYFIFGFSGIFETI 120
 QY 121 LITIDRYLAVVAVFALKARTVTGVTSVITVVAVFASLPGIIFTRSOKEGLHYTCS 180

Dd		121	LITLIDRLVLAIVHAFAFLAKARVRGVTSVTWVAVPASLPGLIIFRRSOREGHLHYCSS	180
Oy		181	HFPYSQIQEFKNEFOTLKAVILGLVPLLVMTCTSGILKTLRLRNRKKRRRAVLFTT	240
Dd		181	HFPYSQIQEFKNEFOTLKAVILGLVPLLVMTCTSGILKTLRLRNRKKRRRAVLFTT	240
Oy		241	MIVYELFWAPNVIYLLNTPOEFFGLNNCCSSNNLDQAMQVTELTGMTHCCINPIYAFAV	300
Dd		241	MIVYELFWAPNVIYLLNTPOEFFGLNNCCSSNNLDQAMQVTELTGMTHCCINPIYAFAV	300
Oy		301	GEFRFNVLVFFQKHIAKRFCCKCSIPFOEAPERASSVYTRSTGEQISVGL	352
Dd		301	GEFRFNVLVFFQKHIAKRFCCKCYIFFOEAPERASSVYTRSTGEQISVGL	352
RESULT 9				
CCKRS_PYGNE				
ID	CCKRS_PYGNE	STANDARD:	PRT:	352 AA.
AC	097882;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	C-C chemokine receptor type 5 (C-C CCR-5) (CC-CRK-5) (CCR-5) (CCR5).			
GN	CCKRS OR CKBKBS.			
OS	Pygaltrix nemaeus (Dove langur).			
OC	Eukaryota; Metazoa; Chordata; Carnivata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;			
OX	Pygaltrix.			
NCBI_Taxid=54133;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99416438; PubMed-10486970;			
RA	Zhang Y.-W., Ryder O.A., Zhang Y.-P.;			
RI	"Sequence evolution of the CCR5 chemokine receptor gene in primates.";			
RL	Mol. Biol. Evol. 16:1145-1154(1999)			
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,			
CC	MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY			
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE			
CC	IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR			
CC	DIFFERENTIATION.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL, AF075448; AAD19860.1. -			
DR	Interpro: IPR000276; GPCR_Rhodpsn.			
DR	pfam: PF00001; 7tm_1; 1.			
DR	PRINTS: PR00237; GPCRRHODOPSN.			
DR	PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.			
DR	PROSITE: PS0262; G_PROTEIN_RECP_FL_2; 1.			
KM	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.			
FT	DOMAIN	1		
FT	TRANSMEM	31		
FT	TRANSMEM	58		
FT	DOMAIN	59		
FT	TRANSMEM	69		
FT	TRANSMEM	88		
FT	DOMAIN	90		
FT	TRANSMEM	103		
FT	TRANSMEM	124		
FT	DOMAIN	125		
FT	TRANSMEM	141		
FT	TRANSMEM	142		
FT	TRANSMEM	167		
FT	TRANSMEM	199		
FT	TRANSMEM	219		
FT	TRANSMEM	235		
FT	TRANSMEM	236		
FT	TRANSMEM	261		
FT	TRANSMEM	277		
FT				

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FT FT DOMAIN 352 352 CYTOPLASMIC (POTENTIAL) .
FT FT DISULFID 101 178 BY SIMILARITY .
FT MOD_RES 3 3 SUTURATION (BY SIMILARITY) .
FT MOD_RES 10 10 SUTURATION (BY SIMILARITY) .
FT MOD_RES 14 14 SUTURATION (BY SIMILARITY) .
FT MOD_RES 15 15 SUTURATION (BY SIMILARITY) .
SQ SEQUENCE 352 AA; 40532 MW; F64FD9D8D3B3E861 CRC64;

Query Match          98.6%; Score 1815; DB 1; Length 352;
Best Local Similarity 97.4%; Pred. No. 2,3e-90;
Matches 343; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1 MDVYSSEPTVIDINTYTSEPCKIKINVKQIAARLPLSLVFISFGVMATYLILNCKR 60
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       1 MDGVSSSTPYDIDYITSEPCCKVANKQIARLARLPPLSLVIFGVTNLVLILNCKR 60
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61 LKSMETDIYLNLAISDLEFLLTVPFMAYAAOMDFGTMKQLLTGLYEIGFSGIFII 120
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       61 LKSMETDIYLNLAISDLEFLLTVPFMAYAAOMDFGTMKQLLTGLYEIGFSGIFII 120
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      121 LLTIIDRYLAIVAAFAFKARTYTGCVTVSVTTWVAFAFSLGIIFRSOREGLHYTCSS 180
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       121 LLTIIDRYLAIVAAFAFKARTYTGCVTVSVTTWVAFAFSLGIIFRTSOREGLHYTCSS 180
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      181 HFPYSQYQYPMKNPQTAKIVILGVLPLLVMIYCISGLIKTLRLCRNEKKRRRAVALIFTI 240
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       181 HFPYSQYQYPMKNPQTAKIVILGVLPLLVMIYCISGLIKTLRLCRNEKKRRRAVALIFTI 240
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      241 MIYVEFLFAPARNIVALLNTFOEFYGLNNCSSSNRIDQAMQYETLGMTCHCINPIIYAFV 300
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       241 MIYVEFLFAPARNIVALLNTPOEFGGLNNCSSSNRIDQAMQYETLGMTCHCINPIIYAFV 300
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      301 GEKERNYLVTFQKHIAKRFCKCSIFQGEAPERASSYTTSTGDEQSIVGL 352
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB       301 GEKERNYLVTFQKHIAKRFCKCSIFQGEAPERASSYTTSTGHEHSIVGL 352
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESU_10
CR5_HYLE
ID CR5_HYLE STANDARD: PRT: 352 AA.
AC 09/883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CCR-5) (CCR-5) (CCR5).
GN Hylobates leucogerys (White-cheeked gibbon).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_Taxid=61853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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or send an email to license@isb-sdb.ch).
EMBL: AF075451; AAD19863.1;

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InterPro: IPRO00276: GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECPT_F2_1; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 88
 FT TRANSMEM 89 102
 FT DOMAIN 103 124
 FT TRANSMEM 125 141
 FT TRANSMEM 142 166
 FT TRANSMEM 167 198
 FT TRANSMEM 199 218
 FT TRANSMEM 219 235
 FT TRANSMEM 236 260
 FT TRANSMEM 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 SQ SEQUENCE 352 AA; 40445 MW; 4F84F344CEB7C91 CRC64;
 Query Match 98.5%; Score 1814; DB 1; Length 352;
 Best Local Similarity 98.3%; Pred. No. 2.6e-90;
 Matches 346; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MDVQSSPIYDINTYSEPCOKINVKOIAARLLPRLYSLVFEGVGNMLVILINCKR 60
 DB 1 MDVQSSPIYDINTYSEPCOKINVKOIAARLLPRLYSLVFEGVGNMLVILINCKR 60
 QY 61 LKMTDLYLNLALISDFELTVPFNAHYAAMDPCNTCOLLTGTYTGFSGIFFI 120
 DB 61 LKMTDLYLNLALISDFELTVPFNAHYAAMDPCNTCOLLTGTYTGFSGIFFI 120
 QY 121 LTTIDRLAVVAVFALKARTVFGVTSVITVVAVFASLPGIIFTRSOKEGLHYTCSS 180
 DB 121 LTTIDRLAVVAVFALKARTVFGVTSVITVVAVFASLPGIIFTRSOKEGLHYTCSS 180
 QY 181 HEPYSQYQFKNFQTKIVLGLVPLVAVICYSGLIKTLRCRNEKKRHRAVRLFTI 240
 DB 181 HEPYSQYQFKNFQTKIVLGLVPLVAVICYSGLIKTLRCRNEKKRHRAVRLFTI 240
 QY 241 MIYFELFAPRYNIVLINTFOEPFGLNCSNRLDOAMQVTEITLGMHCINPIITAFV 300
 DB 241 MIYFELFAPRYNIVLINTFOEPFGLNCSNRLDOAMQVTEITLGMHCINPIITAFV 300
 QY 301 GERFRNYLVFQKHAKRCKCSIFQOEPARASVYTRSTGEDEISVGL 352
 DB 301 GERFRNYLVFQKHAKRCKCSIFQOEPARASVYTRSTGEDEISVGL 352
 RESULT 11
 CKRS_MACMU STANDARD; PRT; 352 AA.
 AC P79436; 002746; (Rel. 35, Last Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Macaca mulatta (Rhesus macaque) (Cynomolgus monkey), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Corcophilinae; Macaca.
 OX NCBI_TaxID=9544, 9541, 9545;
 RN [1]

RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta;
 RX MEDLINE=97184592; PubMed=9032394;
 RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
 RA Newman W., Gerard N., Gerard C., Sodroski J.;
 RT "Utilization of C-C chemokine receptor 5 by the envelope
 RT glycoproteins of a pathogenic simian immunodeficiency virus,
 RT SIVmac239.";
 RL J. Virol. 71:2522-2527(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta; STRAIN=Indian macaque;
 RX MEDLINE=97213934; PubMed=9060623;
 RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
 RT "Genetically divergent strains of simian immunodeficiency virus use
 RT CCR5 as a coreceptor for entry.";
 RL J. Virol. 71:2705-2714(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta;
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amodeo A., Miller K., Dotanz B.J., Endres M.,
 RA Sharpton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Pelzer S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 DR EMBL: U77672; AAC51109.1; -;
 DR EMBL: U73739; AAC51158.1; -;
 DR EMBL: U96762; AAC34132.1; -;
 DR EMBL: AF005660; AAB62554.1; -;
 DR EMBL: AF005661; AAB62555.1; -;
 DR EMBL: AF005662; AAB62556.1; -;
 DR InterPro: IPRO00276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECPT_F2_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 88
 FT TRANSMEM 89 102
 FT DOMAIN 103 124
 FT TRANSMEM 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218

OY 301 GEFERNYLVFQNHIAKRFCKCSIFQGEAPERASSVYTRSTGEQETISVGL 352
 DB 301 GEFERNYLVFQNHIAKRFCKCSIFQGEAPERASSVYTRSTGEQETISVGL 352
 RESULT 13
 CCR5_CERAE STANDARD: PRT: 352 AA.
 ID CCR5_CERAE STANDARD: PRT: 352 AA.
 AC P56493;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5B5.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecinae.
 OC NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=98001387; PubMed=934322;
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT Implicate specific amino acids in infections by simian and human
 RT Immunodeficiency viruses.*;
 RL J. Virol. 71:8642-8656(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
 RT cDNA sequence of African green monkey CCR-5 chemokine receptor
 RT gene.*;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC -----
 DR EMBL: U83324; AAC51795.1; -;
 DR EMBL: U83325; AAC51796.1; -;
 DR EMBL: AB015944; BAA3138.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHOODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
 DR PROSITE: PS02623; G-PROTEIN_RECEP_F1_2; 1.
 KW G-Protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW Polymorphism.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT TRANSMEM 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT TRANSMEM 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT TRANSMEM 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 FT VARIANT 14 14 N -> Y.
 FT VARIANT 352 352 F -> L.
 SQ SEQUENCE 352 AA; 40561 MM; 7F52E90C72EC29A CRC64;
 Query Match 97.2%; Score 1790; DB 1; Length 352;
 Best Local Similarity 97.2%; Pred. No. 4.9e-89;
 Matches 341; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 OY 1 MDYOVSPYIDINNTSPCKINVKQIAALPLPLSLVIFGFGNMLVILINCKR 60
 DB 1 MDYOVSPYIDINNTSPCKINVKQIAALPLPLSLVIFGFGNMLVILINCKR 60
 OY 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFCNTMQLTGLYFIFGFGIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFCNTMQLTGLYFIFGFGIFPII 120
 OY 121 LITDRIYAAVHAAPALKARTVTVGVTSVITWVAAPASLPGIIFTRSQEGLHYTCSS 180
 DB 121 LITDRIYAAVHAAPALKARTVTVGVTSVITWVAAPASLPGIIFTRSQEGLHYTCSS 180
 OY 181 HEPYSOYQFMKFPOTLKIIVIGLVPLVWVICYSGILKTLLRCRNEKRRRAVRLPTI 240
 DB 181 HEPYSOYQFMKFPOTLKIIVIGLVPLVWVICYSGILKTLLRCRNEKRRRAVRLPTI 240
 OY 241 MIYFLFMAPYNIYLLNTFQEPFGLNCCSSNRIDQAOVETLGMTHCCINPIYAFV 300
 DB 241 MIYFLFMAPYNIYLLNTFQEPFGLNCCSSNRIDQAOVETLGMTHCCINPIYAFV 300
 OY 301 GEFERNYLVFQNHIAKRFCKCSIFQGEAPERASSVYTRSTGEQETISVGL 351
 DB 301 GEFERNYLVFQNHIAKRFCKCSIFQGEAPERASSVYTRSTGEQETISVGL 351
 RESULT 14
 CCR5_MOUSE STANDARD: PRT: 354 AA.
 ID CCR5_MOUSE STANDARD: PRT: 354 AA.
 AC P51682; Q61867; P97405; O35313; P97308; O35891;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN CCR5 OR CCR5B5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ; TISSUE=Spleen;
 RX MEDLINE=96205938; PubMed=8631787;
 RA Boring L., Gollig J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
 RA Charo I.F.;
 RT "Molecular cloning and functional expression of murine JE (monocyte
 RT chemoattractant protein 1) and murine macrophage inflammatory protein
 RT 1alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.*";
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=96278910; PubMed=8662890;
 RA Meyer A., Coyte A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "Cloning and characterization of a novel murine macrophage
 RT inflammatory protein-1 alpha receptor.*";
 RL J. Biol. Chem. 271:14445-14451(1996).

[3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/Ola;
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.,
 RL submitted (Dec-1996) to the EMBL/Genbank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN-C57BL/6, and NIH Swiss; TISSUE=Liver, Kidney, and spleen;
 RC MEDLINE=96001387; PubMed=9343222;
 RA Kuhlman S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN-129;
 RC MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharon M., Cen Y.H.,
 RT Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314(1997).
 [6]
 RN SEQUENCE FROM N.A.
 RP Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@sdb.ch).
 CC -----
 DR EMBL; U47036; AAC52454.1; -;
 DR EMBL; X94151; CA63867.1; -;
 DR EMBL; U68565; AAB37273.1; -;
 DR EMBL; U83337; AAC53386.1; -;
 DR EMBL; AF022990; AAC53389.1; -;
 DR EMBL; AF019772; AAB71183.1; -;
 DR EMBL; D83648; BAA12024.1; -;
 DR MGI; 107182; Cmkbr5.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1. 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Polymorphism.
 FT DOMAIN 1 32
 FT TRANSMEM 33 60
 FT DOMAIN 61 70
 FT TRANSMEM 71 91
 FT TRANSMEM 92 104
 FT DOMAIN 105 126
 FT TRANSMEM 127 143
 FT DOMAIN 144 168
 FT TRANSMEM 169 200
 FT DOMAIN 201 220
 FT TRANSMEM 221 237
 FT TRANSMEM 238 262
 FT DOMAIN 263 279
 FT TRANSMEM 280 303
 FT TRANSMEM 304 354
 FT DISULFID 103 180
 BY SIMILARITY.

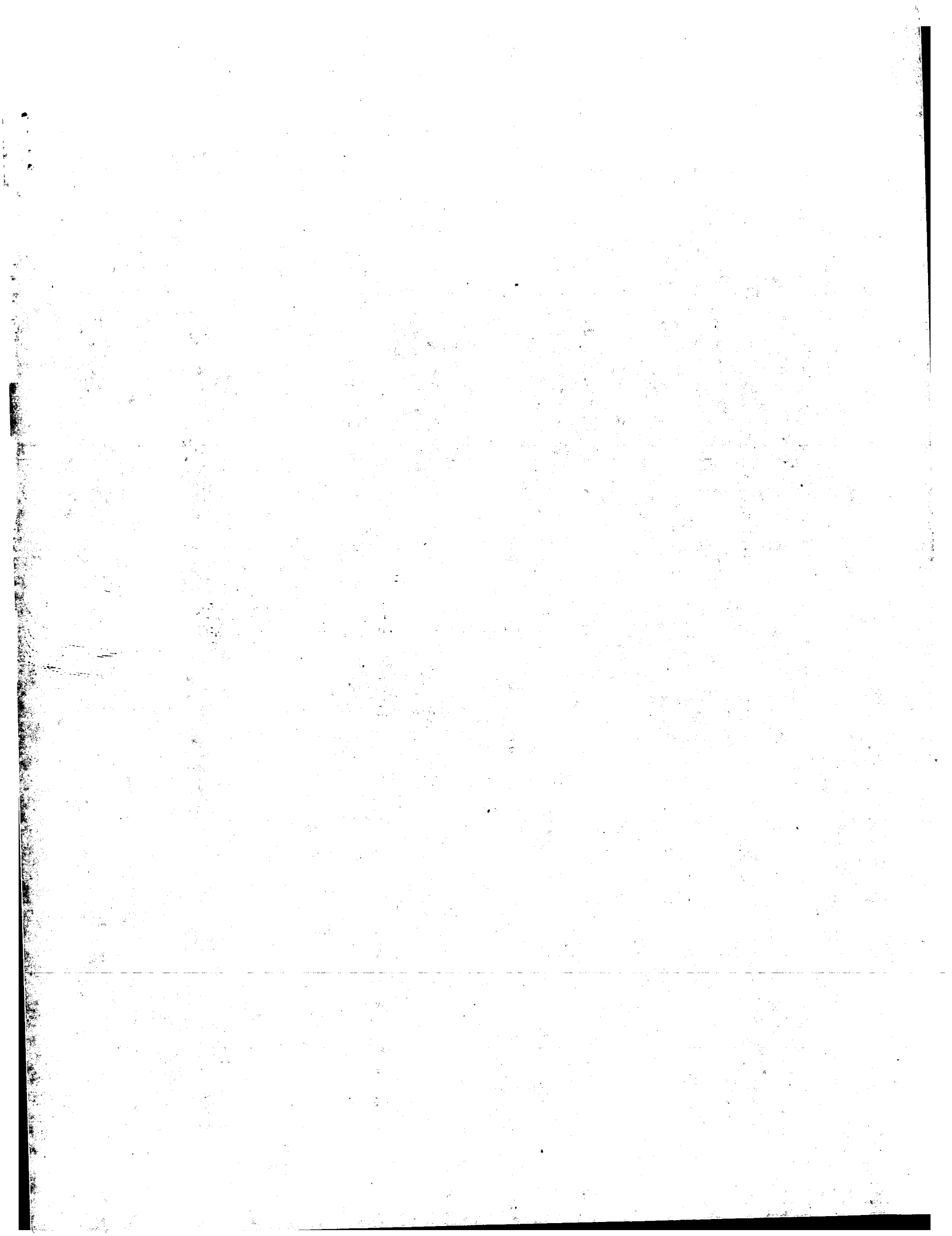
FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 11 11 I -> S.
 FT VARIANT 62 62 K -> R.
 FT VARIANT 66 66 V -> M.
 FT VARIANT 97 97 I -> V.
 FT VARIANT 109 109 V -> L.
 FT VARIANT 156 156 V -> A.
 FT VARIANT 160 160 F -> S.
 FT VARIANT 185 185 P -> L.
 FT VARIANT 213 213 I -> V.
 FT VARIANT 318 318 I -> M.
 FT VARIANT 337 337 V -> A.
 FT VARIANT 3 3 F -> L (IN REF. 2).
 FT CONFLICT 80 80 L -> F (IN REF. 2).
 FT CONFLICT 145 145 N -> I (IN REF. 5).
 FT CONFLICT 190 190 H -> Y (IN REF. 3).
 FT CONFLICT 208 208 P -> S (IN REF. 1).
 SQ SEQUENCE 354 AA: 40863 MW: 84639.4288899CF0 CXC64;
 Query Match 84.5%; Score 1556; DB 1; Length 354;
 Best Local Similarity 81.9%; Pred. No. 1.3e-76;
 Matches 290; Conservative 29; Mismatches 33; Indels 2; Gaps 1;
 QY 1 MDYGVSP--IYDINTYSEPCQKINVAQIARLLPEIXSYFTFGFNGMLVILLINC 58
 DB 1 MDFQGSVPFTYIDIDYDYGNSAPQKINVAQIARLLPEIXSYFTFGFNGMLVILLISC 60
 QY KRLKSMPTDIYLLNLASIDLEFLIVPFAHVAQAQMDGNMCOGLTGLYFGFSGCIF 118
 DB 61 KRLKSVTDIYLLNLASIDLEFLITLPEFAHVAANMIFGNIMCKFTGVYHIGYGCILF 120
 QY 119 ILLTIDRYLAVNAVFAFKATVTEGVVTVIIVVAVASLPGIITFSOKESGHTC 178
 DB 121 ILLTIDRYLAVNAVFAFKATVTEGVVTVIIVVAVASLPGIITFSOKESGHTC 180
 QY 179 SSHPEYSQYQEFWKNQOTKIYVILGLVPLVWVTCYGIITLNCRNKKRAVRLIF 238
 DB 181 SHPEPHQYHFWKSSQTLMAVLSLPLVWVTCYGIITLNCRNKKRAVRLIF 240
 QY 239 TIIIVYFLFWAPYNIIVLLINTEQEFEGGLNCCSSNRDLQAMQVETLGMTGCCIPIT 298
 DB 241 AIMIYVFLFWPYNIIVLLINTEQEFEGGLNCCSSNRDLQAMQVETLGMTGCCIPIT 300
 QY 299 FYGKFRNTLVFPQKHTAKRCCKCSIFQCAPRPASSVYTRSGEDELISGL 352
 DB 301 FYGKFRNTLVFPQKHTAKRCCKCSIFQCAPRPASSVYTRSGEDELISGL 354
 RESULT 15
 CRKS_RAT STANDARD; PRT; 354 AA.
 AC 008556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CR-5) (CC-CR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN CCR5 OR CCKBR5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mistat; TISSUE=Brain;
 RX MEDLINE=98334064; PubMed=9670989;
 RA Spleiss O., Gourmal N., Bodeke H.W.G.M., Sauter A., Fiedlich B.L.,
 RT Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and
 RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
 RL J. Neurosci. Res. 53:16-28(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-Sprague-Dawley;
RA MEDLINE-98318173; Pubmed-9655467;
RA Jlang Y., Salafianca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Delebre C.M., Pennell N.A., Streif W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RL J. Neuroimmunol. 86:1-12(1998).
CC -1- FUNCTION: RECEPTOR FOR A G-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: Y12009; CAA72737.1; -
DR EMBL: U77350; AAC03243.1; -
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1..-
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSSEM 33 60
FT DOMAIN 61 70
FT TRANSSEM 71 91
FT DOMAIN 92 104
FT TRANSSEM 105 126
FT DOMAIN 127 143
FT TRANSSEM 144 168
FT DOMAIN 169 200
FT TRANSSEM 201 220
FT DOMAIN 221 237
FT TRANSSEM 238 262
FT DOMAIN 263 279
FT TRANSSEM 280 303
FT DOMAIN 304 354
FT DISULFID 103 180
FT CARBOHYD 270 270
SQ SEQUENCE 354 AA; 41030 MM; 77EDB368AA4C868D CRC64; . (POTENTIAL).
Query Match 84.0%; Score 1547; DB 1; Length 354;
Best Local Similarity 81.9%; Pred. No. 4e-76;
Matches 290; Conservative 27; Mismatches 35; Indels 2; Gaps 1;
QY 1 MDYGVSSP--YDINVTSEPCORINVKQIARLLPPLYSVFTFGFVGNMLVILILINC 58
DB 1 MDEFGSIPYIYIDIDYSMAKPCQVNVNKOIAQOLPLPLYSVFTFGFVGNMVFLLILISC 60
QY 59 KRLKSMIDYLLNLAIISDLFFLLVFPMAHYAAQWDMGNTMQLTGLYFIFGFSGIF 118
DB 61 KRLKSMIDYLLNLAIISDLFFLLVFPMAHYAAQWDMGNTMQLTGLYFIFGFSGIF 120
QY 119 ILLTIRYLAIVAVPALAKARTYEGVSVITWVAVFASLPGLIIFTRQKGLHTYC 178
DB 121 ILLTIRYLAIVAVPALAKARTYEGVSVITWVAVFASLPGLIIFTRQKGLHTYC 180
QY 179 SSHPEYQYOFKMFOTLKIVILGLVPLVAVICYSGLTLKRCRNEKRHRRAVRLIF 238
DB 181 SPFLNIOYRFKMFOTLKIVILGLVPLVAVICYSGLTLKRCRNEKRHRRAVRLIF 240
QY 239 TIMIVYFLFAPYNIIVLLNTFOEFGLNCSNRLDAQAMQVETLGMTHCCINPIYA 298
DB 241 AIMIVYFLFAPYNIIVLLNTFOEFGLNCSNRLDAQAMQVETLGMTHCCINPIYA 300
QY 299 FVGEKFRNYLLVFFQKRIAKRFCKCSIFQDAEPBRASVYTRSTGEQVSTGL 352

DB

301 FVGEKFRNYLLVFFQKRIAKRFCKCSIFQDAEPBRASVYTRSTGEQVSTGL 354

Search completed: June 3, 2003, 15:19:38
Job time : 21.141 secs



GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 3, 2003, 15:14:58 ; Search time 73.8765 Seconds
(Without alignments)
981.754 Million cell updates/sec

Title: US-09-939-226-5

Perfect score: 1841
Sequence: 1 MDYQVSSPYIDINITYSEPC.....ERASSVYTRSTGEQISVGL 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20647115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1825	99.1	352	6	095NC5
2	1823	99.0	352	6	018771
3	1823	99.0	352	6	018772
4	1822	99.0	352	6	09X599
5	1821	98.9	352	6	09TV50
6	1818	98.8	352	6	095NC7
7	1817	98.7	352	6	095NC8
8	1816	98.6	352	6	095NC8
9	1813	98.5	352	6	097962
10	1812	98.4	352	6	09X714
11	1812	98.4	352	6	095NC1
12	1811	98.4	352	6	095NC6
13	1811	98.4	352	6	095NC3
14	1809	98.3	352	6	09X713
15	1808	98.2	352	6	018770
16	1808	98.2	352	6	0975K1

17	1808	98.2	352	6	09TV49	09TV49 cercopithec
18	1807	98.2	352	6	097975	097975 macaca arc
19	1806	98.1	352	6	09X712	09X712 cercopithec
20	1803	97.9	352	6	09TV42	09TV42 cercopithec
21	1803	97.9	352	6	095NE8	095NE8 cercopithec
22	1803	97.9	352	6	095ND2	095ND2 cercopithec
23	1802	97.9	352	6	077776	077776 mandrillus
24	1802	97.9	352	6	09MZA3	09MZA3 hylobates a
25	1801	97.8	352	6	095ND1	095ND1 mandrillus
26	1800	97.8	352	6	095NE1	095NE1 cercocobus
27	1800	97.8	352	6	095ND0	095ND0 erythrocebu
28	1797	97.6	352	6	09TV93	09TV93 macaca arc
29	1796	97.6	352	6	09TV46	09TV46 cercopithec
30	1795	97.5	352	6	09TOX0	09TOX0 cercopithec
31	1794	97.4	352	6	09BGM5	09BGM5 cercopithec
32	1794	97.4	352	6	09X535	09X535 macaca neme
33	1791	97.3	352	6	09TV43	09TV43 macaca neme
34	1789	97.2	352	6	09TV47	09TV47 cercopithec
35	1789	97.2	352	6	09TS07	09TS07 cercopithec
36	1787	97.1	352	6	09X716	09X716 cercopithec
37	1786	97.0	352	6	09MZA2	09MZA2 cercopithec
38	1784	96.9	352	6	09TV48	09TV48 cercopithec
39	1779	96.6	352	6	09UB99	09UB99 homo sapien
40	1779	96.6	352	6	09TV44	09TV44 cercopithec
41	1776	96.5	339	4	09UN27	09UN27 homo sapien
42	1776	96.5	339	4	09UN37	09UN37 homo sapien
43	1775	96.4	339	4	09UN23	09UN23 homo sapien
44	1774	96.4	339	4	09UN28	09UN28 homo sapien
45	1774	96.4	352	6	09TV45	09TV45 cercopithec

ALIGNMENTS

RESULT 1

ID	095NC5	PRELIMINARY:	PRT:	352 AA.
DT	01-DEC-2001 (TREMBLREL. 19, Created)			
DT	01-DEC-2001 (TREMBLREL. 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLREL. 20, Last annotation update)			
DE	C-C chemokine receptor 5.			
GN	CCR5.			
OS	Hylobates syndactylus (Slamang) (Symphalangus syndactylus).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.			
OX	NCBI_TaxID=9590;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhang Y., Ryder O.A., Zhang Y.;			
RT	*Sequence comparison of the CCR5 gene in primates and primate			
RT	phylogeny.*;			
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF177884; AAK43367.1;			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.			
DR	PROSITE; PS02623; G_PROTEIN_RECEP_F1_2; 1.			
KW	Receptor.			
SO	SEQUENCE			
	352 AA; 40508 MW; FAF64B3AD5AF658A CRC64;			
	Query Match			
	Best Local Similarity			
	98.9%; Pred. No. 9.5e-147;			
	Matches 348; Conservative 2; Mismatches 2; Indels 0; Gaps 0;			

OY	1 MDYQVSSPYIDINITYSEPCOKINVKQIAANLPLVSLVFSGFVGMVILLINCKR 60	
DB	1 MDYQVSSPYIDIDVTSPECKINVKQIAANLPLVSLVFSGFVGMVILLINCKR 60	
OY	61 LKSWTDLYLNLAIASDLEFLLTPFMAHYAAQDFGNTKCOLTGLYTFGFSGIFPII 120	
DB	61 LKSWTDLYLNLAIASDLEFLLTPFMAHYAAQDFGNTKCOLTGLYTFGFSGIFPII 120	

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OY 121 LITIDRYIAVAVFALKAARYTGVTSVITWVAVASLPGLITFRSOKEGHLYTCSS 180
DB 121 LITIDRYIAVAVFALKAARYTGVTSVITWVAVASLPGLITFRSOKEGHLYTCSS 180
OY 181 HEPYSOYOFWKNFOTLKIVILGLVPLVMVICYSGILKTLRCRNEKKRRRAVRLIFTI 240
DB 181 HEPYSOYOFWKNFOTLKIVILGLVPLVMVICYSGILKTLRCRNEKKRRRAVRLIFTI 240
OY 241 MIYVFLFWAPYNIYVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIYAFV 300
DB 241 MIYVFLFWAPYNIYVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIYAFV 300
OY 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352

RESULT 2
O18771 PRELIMINARY; PRT; 352 AA.
AC 018771:
DR 01-JAN-1998 (TREMBLrel. 05, Created)
DR 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHCCRS-141A;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011539; AAB65739.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KM Receptor.
FT NON-TER
SQ SEQUENCE 352 AA; 40466 MW; 3EFFAC7ABAE1DAFB CRC64;

Query Match
Best Local Similarity 99.0%; Score 1823; DB 6; Length 352;
Matches 348; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDVQSSPIYDINTYSEPCOKINVOIAARLLPPLYSVIFGFGVNMVILILINCKR 60
DB 1 MDVQSSPIYDINTYSEPCOKINVOIAARLLPPLYSVIFGFGVNMVILILINCKR 60
OY 61 LKSMTDIYLLNLAISDLFFLLVPPMAHYAAQWDFGNTMQLTGLYIFGFGSIFPTI 120
DB 61 LKSMTDIYLLNLAISDLFFLLVPPMAHYAAQWDFGNTMQLTGLYIFGFGSIFPTI 120
OY 121 LITIDRYIAVAVFALKAARYTGVTSVITWVAVASLPGLITFRSOKEGHLYTCSS 180
DB 121 LITIDRYIAVAVFALKAARYTGVTSVITWVAVASLPGLITFRSOKEGHLYTCSS 180
OY 181 HEPYSOYOFWKNFOTLKIVILGLVPLVMVICYSGILKTLRCRNEKKRRRAVRLIFTI 240
DB 181 HEPYSOYOFWKNFOTLKIVILGLVPLVMVICYSGILKTLRCRNEKKRRRAVRLIFTI 240
OY 241 MIYVFLFWAPYNIYVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIYAFV 300
DB 241 MIYVFLFWAPYNIYVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIYAFV 300
OY 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352

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DB 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352

RESULT 3
O18772 PRELIMINARY; PRT; 352 AA.
AC 018772:
DR 01-JAN-1998 (TREMBLrel. 05, Created)
DR 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHCCRS-142A;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011541; AAB65741.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KM Receptor.
FT NON-TER
SQ SEQUENCE 352 AA; 40598 MW; 39688BA7004C952F CRC64;

Query Match
Best Local Similarity 99.0%; Score 1823; DB 6; Length 352;
Matches 348; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDVQSSPIYDINTYSEPCOKINVOIAARLLPPLYSVIFGFGVNMVILILINCKR 60
DB 1 MDVQSSPIYDINTYSEPCOKINVOIAARLLPPLYSVIFGFGVNMVILILINCKR 60
OY 61 LKSMTDIYLLNLAISDLFFLLVPPMAHYAAQWDFGNTMQLTGLYIFGFGSIFPTI 120
DB 61 LKSMTDIYLLNLAISDLFFLLVPPMAHYAAQWDFGNTMQLTGLYIFGFGSIFPTI 120
OY 121 LITIDRYIAVAVFALKAARYTGVTSVITWVAVASLPGLITFRSOKEGHLYTCSS 180
DB 121 LITIDRYIAVAVFALKAARYTGVTSVITWVAVASLPGLITFRSOKEGHLYTCSS 180
OY 181 HEPYSOYOFWKNFOTLKIVILGLVPLVMVICYSGILKTLRCRNEKKRRRAVRLIFTI 240
DB 181 HEPYSOYOFWKNFOTLKIVILGLVPLVMVICYSGILKTLRCRNEKKRRRAVRLIFTI 240
OY 241 MIYVFLFWAPYNIYVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIYAFV 300
DB 241 MIYVFLFWAPYNIYVLLNTFQEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIYAFV 300
OY 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352
DB 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGEQEIISVGL 352

RESULT 4
O9XS99 PRELIMINARY; PRT; 352 AA.
AC 09XS99:
DR 01-NOV-1999 (TREMBLrel. 12, Created)
DR 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DR 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
ON NCBI_TaxID=9593;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GORILLACR:
RX MEDLINE=99210133; PubMed=10195758;
RA Sakeena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lai R.B.:
RT "Species-specific changes in the CCR5 gene from African and Asian
RL nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
DR EMBL: AF105291; AD020560.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40529 MW; 1BE6C68FE2E7AD0 CRC64;

Query Match 99.0%; Score 1822; DB 6; Length 352;
Best Local Similarity 98.6%; Pred. No. 1,7e-146;
Matches 347; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDYOVSSPIYDINVTSEPOKINVKQIAARLLPPLSLVIFGFVGNMVLILINCKR 60
DB 1 MDYOVSSPTDIDITSEPOKINVKQIAARLLPPLSLVIFGFVGNMVLILINCKR 60
OY 61 LKSWTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPGNTMQLTGLYFIFGSGIFPII 120
DB 61 LKSWTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPGNTMQLTGLYFIFGSGIFPII 120
OY 121 LITDRILAVYHAFALKARTVFGVTSVTWVAVFASLPGIIFTRSGEGHLYTCS 180
DB 121 LITDRILAVYHAFALKARTVFGVTSVTWVAVFASLPGIIFTRSGEGHLYTCS 180
OY 181 HEPYSOYOFMKNFOTLKIIVILGLVPLVNYICVSGILKTLRCRNEKKRRARLFTI 240
DB 181 HEPYSOYOFMKNFOTLKIIVILGLVPLVNYICVSGILKTLRCRNEKKRRARLFTI 240
OY 241 MIVFLFMAPYNIYLLNTFOEPFGLNCCSSNNLDQAMQVETLGMTHCCINPIIYAFV 300
DB 241 MIVFLFMAPYNIYLLNTFOEPFGLNCCSSNNLDQAMQVETLGMTHCCINPIIYAFV 300
OY 301 GEKRNILVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKRNILVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 5
OY 09TV50 PRELIMINARY; PRT; 352 AA.
ID 09TV50
AC 09TV50;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-1410;
RX MEDLINE=99335215; PubMed=10408730;
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RT "Mutations in CCR5-coding sequences are not associated with HIV
RL carrier status in African nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-1410;

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RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RC Georges-Courbot M.-C., Barre-Sinoussi F., Fomsgaard A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF035214; AA044007.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40481 MW; 2578A0FC2074A65 CRC64;

Query Match 98.9%; Score 1821; DB 6; Length 352;
Best Local Similarity 98.3%; Pred. No. 2.1e-146;
Matches 346; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYOVSSPIYDINVTSEPOKINVKQIAARLLPPLSLVIFGFVGNMVLILINCKR 60
DB 1 MDYOVSSPTDIDITSEPOKINVKQIAARLLPPLSLVIFGFVGNMVLILINCKR 60
OY 61 LKSWTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPGNTMQLTGLYFIFGSGIFPII 120
DB 61 LKSWTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPGNTMQLTGLYFIFGSGIFPII 120
OY 121 LITDRILAVYHAFALKARTVFGVTSVTWVAVFASLPGIIFTRSGEGHLYTCS 180
DB 121 LITDRILAVYHAFALKARTVFGVTSVTWVAVFASLPGIIFTRSGEGHLYTCS 180
OY 181 HEPYSOYOFMKNFOTLKIIVILGLVPLVNYICVSGILKTLRCRNEKKRRARLFTI 240
DB 181 HEPYSOYOFMKNFOTLKIIVILGLVPLVNYICVSGILKTLRCRNEKKRRARLFTI 240
OY 241 MIVFLFMAPYNIYLLNTFOEPFGLNCCSSNNLDQAMQVETLGMTHCCINPIIYAFV 300
DB 241 MIVFLFMAPYNIYLLNTFOEPFGLNCCSSNNLDQAMQVETLGMTHCCINPIIYAFV 300
OY 301 GEKRNILVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKRNILVFFQKHAKRCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 6
OY 095NCO PRELIMINARY; PRT; 352 AA.
ID 095NCO
AC 095NCO;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates moloch (silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RL phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF177899; AA03382.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CE274 CRC64;

Query Match 98.8%; Score 1818; DB 6; Length 352;
Best Local Similarity 98.6%; Pred. No. 3.7e-146;
Matches 347; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MDYOVSSPIYDINVTSEPOKINVKQIAARLLPPLSLVIFGFVGNMVLILINCKR 60

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DB 1 MDQVSSPTDYDITSEPCQKINVKQIARLLPLYSIVTFEGVGNMVLILINCKR 60
QY 61 LKSMTDIYLLNLAISDFELLVPPWAHYAAQWDEGNTMQLTGLYTFGFSGIFETI 120
DB 61 LKSMTDIYLLNLAISDFELLVPPWAHYAAQWDEGNTMQLTGLYTFGFSGIFETI 120
QY 121 LTTIDRYLAIVAAVAFKARVTFEGVTSVITWVAVAFSLPGIIFTRSQEGHAYTCS 180
DB 121 LTTIDRYLAIVAAVAFKARVTFEGVTSVITWVAVAFSLPGIIFTRSQEGHAYTCS 180
QY 181 HEPYSOYOFWKNFQTLKIYILGLVPLVAVICSGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HEPYSOYOFWKNFQTLKIYILGLVPLVAVICSGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYELFMAPYNIIVLLNTFOEFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
DB 241 MIVYELFMAPYNIIVLLNTFOEFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
QY 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352
DB 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352

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RESULT 7

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QY 095NC7 PRELIMINARY; PRT; 352 AA.
AC 095NC7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Nasalis larvatus (Proboscis monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Nasalis.
ON NCBI_TaxID=43780;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny."
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177882; AAK43365.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
DR RECEPTOR.
KW SEQUENCE.
SQ SEQUENCE 352 AA; 40537 MW; 51F6F1486E35938E CRC64;

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Query Match 98.7%; Score 1817; DB 6; Length 352;
 Best Local Similarity 97.7%; Pred. No. 4.5e-146;
 Matches 344; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MDQVSSPTDYDITSEPCQKINVKQIARLLPLYSIVTFEGVGNMVLILINCKR 60
DB 1 MDQVSSPTDYDITSEPCQKINVKQIARLLPLYSIVTFEGVGNMVLILINCKR 60
QY 61 LKSMTDIYLLNLAISDFELLVPPWAHYAAQWDEGNTMQLTGLYTFGFSGIFETI 120
DB 61 LKSMTDIYLLNLAISDFELLVPPWAHYAAQWDEGNTMQLTGLYTFGFSGIFETI 120
QY 121 LTTIDRYLAIVAAVAFKARVTFEGVTSVITWVAVAFSLPGIIFTRSQEGHAYTCS 180
DB 121 LTTIDRYLAIVAAVAFKARVTFEGVTSVITWVAVAFSLPGIIFTRSQEGHAYTCS 180
QY 181 HEPYSOYOFWKNFQTLKIYILGLVPLVAVICSGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HEPYSOYOFWKNFQTLKIYILGLVPLVAVICSGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYELFMAPYNIIVLLNTFOEFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300

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DB 241 MIVYELFMAPYNIIVLLNTFOEFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
QY 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352
DB 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352

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RESULT 8

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QY 095NC8 PRELIMINARY; PRT; 352 AA.
AC 095NC8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Colobus polykomos.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
ON NCBI_TaxID=9572;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny."
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177881; AAK43364.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
DR RECEPTOR.
KW SEQUENCE.
SQ SEQUENCE 352 AA; 40578 MW; 4366F149C3B4938F CRC64;

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Query Match 98.6%; Score 1816; DB 6; Length 352;
 Best Local Similarity 97.7%; Pred. No. 5.5e-146;
 Matches 344; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MDQVSSPTDYDITSEPCQKINVKQIARLLPLYSIVTFEGVGNMVLILINCKR 60
DB 1 MDQVSSPTDYDITSEPCQKINVKQIARLLPLYSIVTFEGVGNMVLILINCKR 60
QY 61 LKSMTDIYLLNLAISDFELLVPPWAHYAAQWDEGNTMQLTGLYTFGFSGIFETI 120
DB 61 LKSMTDIYLLNLAISDFELLVPPWAHYAAQWDEGNTMQLTGLYTFGFSGIFETI 120
QY 121 LTTIDRYLAIVAAVAFKARVTFEGVTSVITWVAVAFSLPGIIFTRSQEGHAYTCS 180
DB 121 LTTIDRYLAIVAAVAFKARVTFEGVTSVITWVAVAFSLPGIIFTRSQEGHAYTCS 180
QY 181 HEPYSOYOFWKNFQTLKIYILGLVPLVAVICSGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HEPYSOYOFWKNFQTLKIYILGLVPLVAVICSGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYELFMAPYNIIVLLNTFOEFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
DB 241 MIVYELFMAPYNIIVLLNTFOEFGLNCCSSNRDLQAMQVETLGMTHCCINPIIYAV 300
QY 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352
DB 301 GEFERNYLLVFQKHAKRFCKCSIFQOEAPERASSVYTRSTGEOEISVGL 352

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CN CCR5.
 OS Pygathrix ayuunculus (Tonkin snub-nosed monkey), and
 OS Pygathrix foxellana (golden snub-nosed monkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 NCBI_TaxID=66062, 61622;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y.-W., Zhang Y.-P.;
 RT "Sequence evolution of chemokine receptor CCR5 gene in primates."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF075447; AAD19859.1;
 DR EMBL: AF075444; AAD19856.1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40482 MW; 037CFA9E12E532E3 CRC64;
 Query Match 98.4%; Score 1813; DB 6; Length 352;
 Best Local Similarity 97.4%; Pred. No. 9, 8e-146; Mismatches 2; Indels 0; Gaps 0;
 Matches 343; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDVQSSPTIDINTYSEPCOKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
 DB 1 MDVQSSPTIDINTYSEPCOKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
 QY 61 LKMTDYLNLNLAISDFLLTVPFMAHYAAQMDPNTMCOILLTGIFGFSGIFPII 120
 DB 61 LKMTDYLNLNLAISDFLLTVPFMAHYAAQMDPNTMCOILLTGIFGFSGIFPII 120
 QY 121 LFTIDRYLAVHAAVFAFKARTVFGVTVSTTWVAVFASLPGIIFTRSQEGILHYCCS 180
 DB 121 LFTIDRYLAVHAAVFAFKARTVFGVTVSTTWVAVFASLPGIIFTRSQEGILHYCCS 180
 QY 181 HFPYSQYQFKNFOTLKIIVILGLVPLLVNVCISGLIKTLRCRNEKKRRRAVRLFTI 240
 DB 181 HFPYSQYQFKNFOTLKIIVILGLVPLLVNVCISGLIKTLRCRNEKKRRRAVRLFTI 240
 QY 241 MIYFLEMAPYNIYLLNTFOEFGNLCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 DB 241 MIYFLEMAPYNIYLLNTFOEFGNLCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 QY 301 GEFKNYLLVFFOKHIAKRCCKCSIFQEAPEBASVYTRSTGEQISVGL 352
 DB 301 GEFKNYLLVFFOKHIAKRCCKCSIFQEAPEBASVYTRSTGEQISVGL 352
 RESULT 10
 Q9XT14 PRELIMINARY; PRT; 352 AA.
 ID Q9XT14
 AC Q9XT14
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CC chemokine receptor 5.
 GN CCR5.
 OS Colobus guereza (Black-and-white colobus monkey).
 OC Eukaryota; Metazoa; Chordata; Catarrhini; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Colobus.
 NCBI_TaxID=33548;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Spectator P.W., Mburu D.N., Graham B.S.;
 RT "Differential utilization of CCR5 molecules from Three East African
 RT Simian Species by the HIV-1 Envelope Glycoprotein."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF141639; AAD32684.1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40550 MW; 9B078EFD04D3BD36 CRC64;
 Query Match 98.4%; Score 1812; DB 6; Length 352;
 Best Local Similarity 97.4%; Pred. No. 1.2e-145; Mismatches 3; Indels 0; Gaps 0;
 Matches 343; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MDVQSSPTIDINTYSEPCOKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
 DB 1 MDVQSSPTIDINTYSEPCOKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
 QY 61 LKMTDYLNLNLAISDFLLTVPFMAHYAAQMDPNTMCOILLTGIFGFSGIFPII 120
 DB 61 LKMTDYLNLNLAISDFLLTVPFMAHYAAQMDPNTMCOILLTGIFGFSGIFPII 120
 QY 121 LFTIDRYLAVHAAVFAFKARTVFGVTVSTTWVAVFASLPGIIFTRSQEGILHYCCS 180
 DB 121 LFTIDRYLAVHAAVFAFKARTVFGVTVSTTWVAVFASLPGIIFTRSQEGILHYCCS 180
 QY 181 HFPYSQYQFKNFOTLKIIVILGLVPLLVNVCISGLIKTLRCRNEKKRRRAVRLFTI 240
 DB 181 HFPYSQYQFKNFOTLKIIVILGLVPLLVNVCISGLIKTLRCRNEKKRRRAVRLFTI 240
 QY 241 MIYFLEMAPYNIYLLNTFOEFGNLCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 DB 241 MIYFLEMAPYNIYLLNTFOEFGNLCSSNNRLDQAMOVETLGMTHCCINPIIYAFV 300
 QY 301 GEFKNYLLVFFOKHIAKRCCKCSIFQEAPEBASVYTRSTGEQISVGL 352
 DB 301 GEFKNYLLVFFOKHIAKRCCKCSIFQEAPEBASVYTRSTGEQISVGL 352
 RESULT 11
 Q95NC1 PRELIMINARY; PRT; 352 AA.
 ID Q95NC1
 AC Q95NC1
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5.
 GN CCR5.
 OS Theropithecus gelada (Gelada baboon).
 OC Eukaryota; Metazoa; Chordata; Catarrhini; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Theropithecus.
 NCBI_TaxID=9565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF177891; AAK43374.1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40475 MW; 4D3643BC13E90D5 CRC64;
 Query Match 98.4%; Score 1812; DB 6; Length 352;
 Best Local Similarity 97.7%; Pred. No. 1.2e-145; Mismatches 3; Indels 0; Gaps 0;
 Matches 344; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MDVQSSPTIDINTYSEPCOKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
 DB 1 MDVQSSPTIDINTYSEPCOKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
 QY 61 LKMTDYLNLNLAISDFLLTVPFMAHYAAQMDPNTMCOILLTGIFGFSGIFPII 120

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Db      61 LKSMIDYILNLAISDLFLTLVPEWAAHAAQMDGNTMCOLLTLGLYFIFGFSGIFETI 120
      121 LITIDRYLAVAVAFALKARTYFGVYTSVITWVAVFASLPGIITFRSQREGHAYTCSS 180
      121 LITIDRYLAVAVAFALKARTYFGVYTSVITWVAVFASLPGIITFRSQREGHAYTCSS 180
      181 HEPYSOYQWKNFQTLKIVILGLVPLVMVICYSGLTKTLRCRNEKKRHRVRLIFTI 240
      181 HEPYSOYQWKNFQTLKIVILGLVPLVMVICYSGLTKTLRCRNEKKRHRVRLIFTI 240
      241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAAQVETLGMTCCINPIITAYV 300
      241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAAQVETLGMTCCINPIITAYV 300
      301 GEKFRNYLLVFQKHIAKRFCKCSIFQOEAPERASSVYTRSGEOEISVGL 352
      301 GEKFRNYLLVFQKHIAKRFCKCSIFQOEAPERASSVYTRSGEOEISVGL 352

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RESULT 12

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ID      095NC6      PRELIMINARY;      PRT;      352 AA.
AC      095NC6:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      C-C chemokine receptor 5.
GN      CCR5.
OS      Trachypithecus johnii (hooded leaf monkey).
OC      Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;
OC      Trachypithecus.
OX      NCBI_Taxid=66063;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang Y., Ryder O.A., Zhang Y.;
RT      "Sequence comparison of the CCR5 gene in primates and primate
RT      phylogeny.";
RL      Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF177883; AAK43366.1;
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm.1; 1.
DR      PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR      PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW      Receptor.
SQ      SEQUENCE 352 AA; 40462 MW; 52824E032259E7F CRC64;

```

Query Match 98.4%; Score 1811; DB 6; Length 352;

Best Local Similarity 97.4%; Pred. No. 1.5e-145;

Matches 343; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

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      1 MDYOVSSPYIDINVTYSEPCOKINVKQIARLLPLYSLVFTFGFVGNMLVTLILNCR 60
      1 MDYOVSSPYIDINVTYSEPCOKINVKQIARLLPLYSLVFTFGFVGNMLVTLILNCR 60
      61 LKSMIDYILNLAISDLFLTLVPEWAAHAAQMDGNTMCOLLTLGLYFIFGFSGIFETI 120
      61 LKSMIDYILNLAISDLFLTLVPEWAAHAAQMDGNTMCOLLTLGLYFIFGFSGIFETI 120
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Db      301 GEKFRNYLLVFQKHIAKRFCKCSIFQOEAPERASSVYTRSGEOEISVGL 352

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RESULT 13

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ID      095NC3      PRELIMINARY;      PRT;      352 AA.
AC      095NC3:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      C-C chemokine receptor 5.
GN      CCR5.
OS      Mopithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC      Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC      Cercopitheciinae; Mopithecus.
OX      NCBI_Taxid=36231;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang Y., Ryder O.A., Zhang Y.;
RT      "Sequence comparison of the CCR5 gene in primates and primate
RT      phylogeny.";
RL      Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF177883; AAK43369.1;
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm.1; 1.
DR      PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR      PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
KW      Receptor.
SQ      SEQUENCE 352 AA; 40546 MW; 6464152F3E566A5 CRC64;

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Query Match 98.4%; Score 1811; DB 6; Length 352;

Best Local Similarity 97.7%; Pred. No. 1.5e-145;

Matches 344; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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      241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAAQVETLGMTCCINPIITAYV 300
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RESULT 14

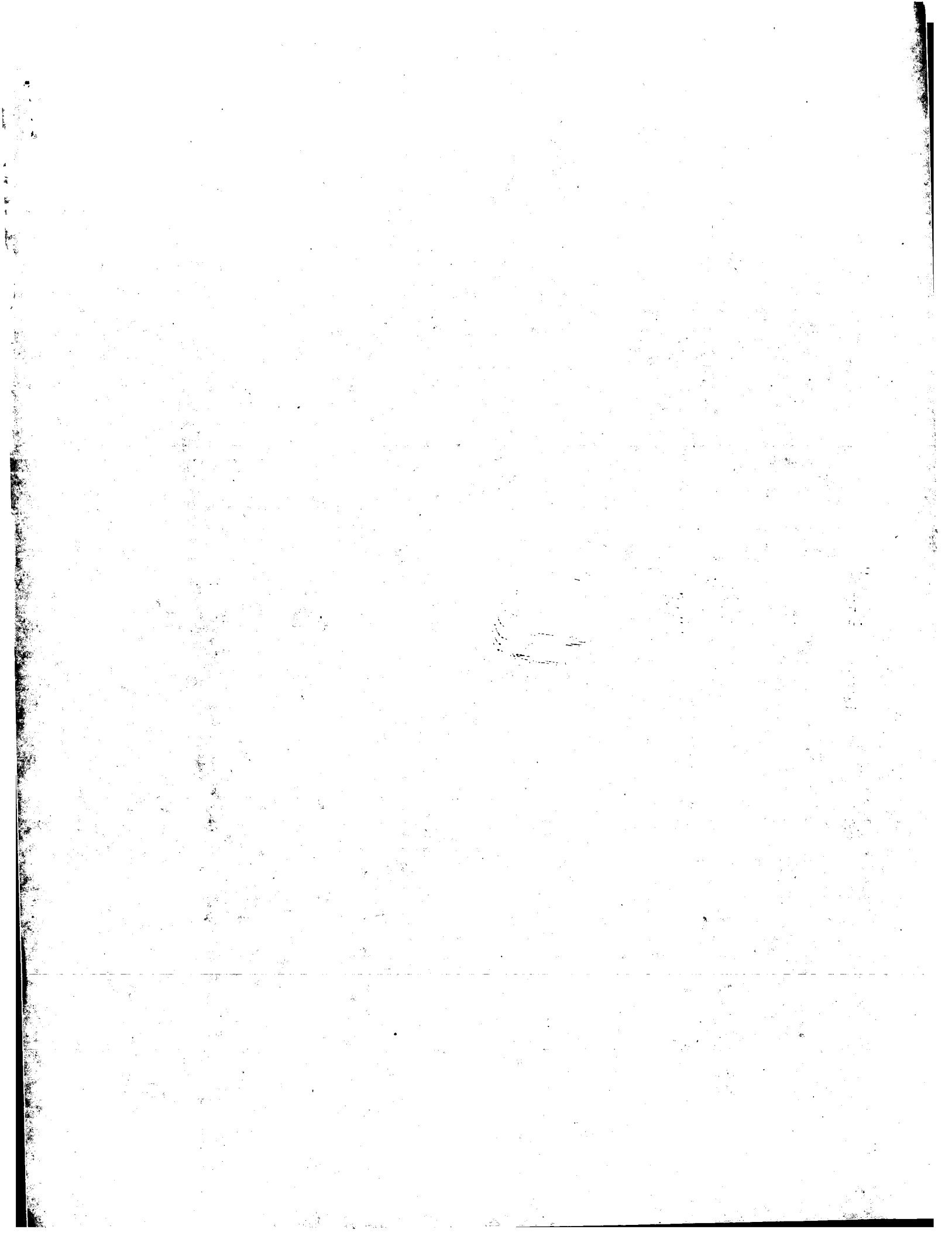
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DT      01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      CC chemokine receptor 5.
GN      CCR5.
OS      Papio anubis (Olive baboon).
OC      Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

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CC Carcophthorinae; Papio.
 OK NCBI_TaxID=9555;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Spearman P.M., Mburu D.N., Graham B.S.:
 RT "Differential utilization of CCR5 molecules from three East African
 RT human species by the HIV-1 Envelope Glycoprotein."
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF11640; AAD32685.1;
 DR InterPro: IPR000376; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECIP_F1_2; 1.
 DR Receptor.
 SQ SEQUENCE 352 AA; 40489 MW; 0847E337C11E2E1E CRC64;
 Query Match 98.3%; Score 1809; DB 6; Length 352;
 Best Local Similarity 97.7%; Pred. No. 2.1e-145;
 Matches 343; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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 DB 1 MDQVSSPIYDIDYTTSPCKINVKQIAARLLPPLVSLVFIKFGVGNLVLLINCKR 60
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 DB 61 LKSMIDYLLNLAIISDLFFLLTPFPMAYAAQMDFGNTKCOLTGLYFIFGFSGIFPII 120
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 DB 121 LITIDRYLAIVHAAVFAKARTVTCGVTSVITWVAVASLPGIIFTSORGLHYTCSS 180
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 DB 181 HEPYSQYOFMKNFOTLKIVILGLVPLPLVWVICYSGILKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIVYFLFAPYNIYVLLNTFOEFGLNCCSSNRIDQAMQVETLGMTHCCINPIYAVF 300
 DB 241 MIVYFLFAPYNIYVLLNTFOEFGLNCCSSNRIDQAMQVETLGMTHCCINPIYAVF 300
 QY 301 GEKFNNTLVFFOKHIAKRFCKCSIFQOEAPERASSVYTRSTGEOETISVGL 352
 DB 301 GEKFNNTLVFFOKHIAKRFCKCSIFQOEAPERASSVYTRSTGEOETISVGL 352
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 AC 018770;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CCR5 receptor (Fragment).
 CN CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_TaxID=9598;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MACCR5-140A;
 RA Zhang L., Cartuthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
 DR EMBL; AF011538; AAB65738.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECIP_F1_2; 1.
 KW Receptor.

FT NON_TER 352 352
 SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;
 Query Match 98.2%; Score 1808; DB 6; Length 352;
 Best Local Similarity 97.4%; Pred. No. 2.6e-145;
 Matches 343; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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 DB 1 MDQVSSPIYDIDYTTSPCKINVKQIAARLLPPLVSLVFIKFGVGNLVLLINCKR 60
 QY 61 LKSMIDYLLNLAIISDLFFLLTPFPMAYAAQMDFGNTKCOLTGLYFIFGFSGIFPII 120
 DB 61 LKSMIDYLLNLAIISDLFFLLTPFPMAYAAQMDFGNTKCOLTGLYFIFGFSGIFPII 120
 QY 121 LITIDRYLAIVHAAVFAKARTVTCGVTSVITWVAVASLPGIIFTSORGLHYTCSS 180
 DB 121 LITIDRYLAIVHAAVFAKARTVTCGVTSVITWVAVASLPGIIFTSORGLHYTCSS 180
 QY 181 HEPYSQYOFMKNFOTLKIVILGLVPLPLVWVICYSGILKTLRCNKKRRRAVRLIFTI 240
 DB 181 HEPYSQYOFMKNFOTLKIVILGLVPLPLVWVICYSGILKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIVYFLFAPYNIYVLLNTFOEFGLNCCSSNRIDQAMQVETLGMTHCCINPIYAVF 300
 DB 241 MIVYFLFAPYNIYVLLNTFOEFGLNCCSSNRIDQAMQVETLGMTHCCINPIYAVF 300
 QY 301 GEKFNNTLVFFOKHIAKRFCKCSIFQOEAPERASSVYTRSTGEOETISVGL 352
 DB 301 GEKFNNTLVFFOKHIAKRFCKCSIFQOEAPERASSVYTRSTGEOETISVGL 352
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 Job time : 75.8765 secs



GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 3, 2003, 15:21:53 ; Search time 36.6279 Seconds

(Without alignments)
972.777 Million cell updates/sec.

Title: US-09-939-226-5

Perfect score: 1841
Sequence: 1 MDYOVSSPIYDINVTSEPC.....ERASSYVTSSTGEQETSVGL 352Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA.*

- 1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1841	100.0	352	9	US-10-086-814-1
2	1841	100.0	352	9	US-09-734-221A-14
3	1841	100.0	352	10	US-09-759-841-2
4	1841	100.0	352	10	US-09-813-653-15
5	1841	100.0	352	10	US-09-796-202-1
6	1841	100.0	352	10	US-09-938-719-5
7	1841	100.0	352	10	US-09-939-226-5
8	1841	100.0	352	10	US-09-938-703-5
9	1841	100.0	352	12	US-10-106-623-2
10	1835	99.7	352	10	US-09-813-653-17
11	1833	99.6	352	9	US-10-232-686-2
12	1833	99.6	352	10	US-09-725-285-2
13	1833	99.6	352	10	US-09-779-879A-22
14	1833	99.6	352	10	US-09-779-880A-22
15	1833	99.6	352	10	US-09-195-662A-2
16	1833	99.6	352	10	US-09-339-912A-2
17	1833	99.6	352	10	US-09-502-783A-2
18	1826	99.2	352	10	US-09-779-879A-2
19	1826	99.2	352	10	US-09-779-880A-2

20	1807	98.2	352	12	US-10-106-623-20	Sequence 20, App1
21	1365	74.1	360	10	US-09-131-827A-20	Sequence 20, App1
22	1364	74.1	347	10	US-09-104-792-3	Sequence 3, App1
23	1364	74.1	360	10	US-09-131-827A-2	Sequence 2, App1
24	1350	73.3	360	10	US-09-938-719-7	Sequence 7, App1
25	1350	73.3	360	10	US-09-939-226-7	Sequence 7, App1
26	1350	73.3	360	10	US-09-938-703-7	Sequence 7, App1
27	1224	66.5	344	9	US-10-232-686-9	Sequence 9, App1
28	1224	66.5	344	10	US-09-779-880A-9	Sequence 9, App1
29	1224	66.5	344	10	US-09-725-285-9	Sequence 9, App1
30	1138.5	61.8	329	10	US-09-195-662A-9	Sequence 9, App1
31	1138.5	61.8	329	10	US-09-339-912A-9	Sequence 9, App1
32	1138.5	61.8	329	10	US-09-502-783A-9	Sequence 9, App1
33	1138.5	61.8	355	10	US-09-961-068-1	Sequence 1, App1
34	1055	57.3	355	10	US-09-960-547-1	Sequence 1, App1
35	1055	57.3	375	9	US-10-219-834-78	Sequence 78, App1
36	1055	57.3	355	10	US-09-938-719-9	Sequence 9, App1
37	1028	55.8	355	10	US-09-939-226-9	Sequence 9, App1
38	1028	55.8	355	10	US-09-938-703-9	Sequence 9, App1
39	1028	55.8	355	10	US-09-938-719-4	Sequence 4, App1
40	958	52.0	184	10	US-09-939-226-4	Sequence 4, App1
41	958	52.0	184	10	US-09-938-703-4	Sequence 4, App1
42	958	52.0	215	10	US-09-939-226-6	Sequence 6, App1
43	958	52.0	215	10	US-09-938-719-6	Sequence 6, App1
44	958	52.0	215	10	US-09-939-226-6	Sequence 6, App1
45	958	52.0	215	10	US-09-938-703-6	Sequence 6, App1

ALIGNMENTS

RESULT 1
US-10-086-814-1
Sequence 1, Application US/10086814
Publication No. US20030092632A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086, 814
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 1841; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	LKSWTDIYLLNLAIISDLFFLITVPFMAHYAAQMDPNTWCQILTGILYFGFSGTFFI	120
QY	121	LLTIDRYLAVVAVFALKARTVFGVVTSYITVVAVFASLPGITFRSKEGLHYTCSS	180
DB	121	LLTIDRYLAVVAVFALKARTVFGVVTSYITVVAVFASLPGITFRSKEGLHYTCSS	180
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DB 301 GKKFNRYLLVFOKHIARFKCCSIFQOEAERASSVYTRSTGEOISVGL 352

RESULT 2

US-09-734-221A-14

Sequence 14, Application US/09734221A
Publication No. US20030096221A1

GENERAL INFORMATION:

APPLICANT: LITTMAN, DAN R.

DENG, HONGKUI

ELMEIER, WILFRIED

LANDAU, NATHANIEL R.

LID, KONG

TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH

MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC

USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSER: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/734, 221A

FILING DATE: 11-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/666,020

FILING DATE: 19-JUN-1996

APPLICATION NUMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-004 N2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-734-221A-14

Query Match 100.0%; Score 1841; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.8e-150;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 LITIDRYLAVVAHVAFAKARVTFGVMTSVITWVAFAASLPGLIFTRSOKEGLHYTCSS 180
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RESULT 3

US-09-759-841-2

Sequence 2, Application US/09759841
Patent No. US20010039026A1

GENERAL INFORMATION:

APPLICANT: Rickett, Graham A

APPLICANT: Dobbs, Susan

APPLICANT: Petros, Manoussos

TITLE OF INVENTION: Assay Method

FILE REFERENCE: PC10348APME

CURRENT APPLICATION NUMBER: US/09/759, 841

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: GB 0000661.9

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: GB 0000663.5

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: GB 0000659.3

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 352

TYPE: PRT

ORGANISM: Homo sapiens

US-09-759-841-2

Query Match 100.0%; Score 1841; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.8e-150;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 LITIDRYLAVVAHVAFAKARVTFGVMTSVITWVAFAASLPGLIFTRSOKEGLHYTCSS 180
DB 121 LITIDRYLAVVAHVAFAKARVTFGVMTSVITWVAFAASLPGLIFTRSOKEGLHYTCSS 180
QY 181 HEPYSQYQFWKNFQTKIYIIGLVPLPLVMVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
DB 181 HEPYSQYQFWKNFQTKIYIIGLVPLPLVMVICYSGILKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLFMAPIYIVILLNTFOEFGFLNCCSSNRDQAMQVETIGMTHCCINPIIYAFV 300
DB 241 MIVYFLFMAPIYIVILLNTFOEFGFLNCCSSNRDQAMQVETIGMTHCCINPIIYAFV 300
QY 301 GKKFNRYLLVFOKHIARFKCCSIFQOEAERASSVYTRSTGEOISVGL 352
DB 301 GKKFNRYLLVFOKHIARFKCCSIFQOEAERASSVYTRSTGEOISVGL 352

RESULT 4
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nealon, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 1841; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLNCKR 60
DB 1 MDYVSSPIYDINITYSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLNCKR 60
QY 61 LKSMTDIYLLNLISDLFFLLTVPMHVAQAQMDRGNTMCLLTGLTGFSGIFETI 120
DB 61 LKSMTDIYLLNLISDLFFLLTVPMHVAQAQMDRGNTMCLLTGLTGFSGIFETI 120
QY 121 LTTIDRYLAVHVAFAKARTVTCVTVSYTWVAFAFSLPGIIFRSOKEGLHYTCSS 180
DB 121 LTTIDRYLAVHVAFAKARTVTCVTVSYTWVAFAFSLPGIIFRSOKEGLHYTCSS 180
QY 181 HPEYSOYQFKNFOTLKIYVILGLVPLLVNVCYSGILKTLRCRNEKKRRHRAVRLIFTI 240
DB 181 HPEYSOYQFKNFOTLKIYVILGLVPLLVNVCYSGILKTLRCRNEKKRRHRAVRLIFTI 240
QY 241 MIYFLEMAAPYNTVLLNTFOEFFGLNCCSSNRDLQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIYFLEMAAPYNTVLLNTFOEFFGLNCCSSNRDLQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GERFRNLLVFPQKHIAKRCCKCSIFQDAPEPRASSVYTRSGEODISVGL 352
DB 301 GERFRNLLVFPQKHIAKRCCKCSIFQDAPEPRASSVYTRSGEODISVGL 352

RESULT 5
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Draglic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRF
; ORGANISM: human

US-09-796-202-1
Query Match 100.0%; Score 1841; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLNCKR 60
DB 1 MDYVSSPIYDINITYSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLNCKR 60
QY 61 LKSMTDIYLLNLISDLFFLLTVPMHVAQAQMDRGNTMCLLTGLTGFSGIFETI 120
DB 61 LKSMTDIYLLNLISDLFFLLTVPMHVAQAQMDRGNTMCLLTGLTGFSGIFETI 120
QY 121 LTTIDRYLAVHVAFAKARTVTCVTVSYTWVAFAFSLPGIIFRSOKEGLHYTCSS 180
DB 121 LTTIDRYLAVHVAFAKARTVTCVTVSYTWVAFAFSLPGIIFRSOKEGLHYTCSS 180
QY 181 HPEYSOYQFKNFOTLKIYVILGLVPLLVNVCYSGILKTLRCRNEKKRRHRAVRLIFTI 240
DB 181 HPEYSOYQFKNFOTLKIYVILGLVPLLVNVCYSGILKTLRCRNEKKRRHRAVRLIFTI 240
QY 241 MIYFLEMAAPYNTVLLNTFOEFFGLNCCSSNRDLQAMQVETLGTHTCCINPIIYAFV 300
DB 241 MIYFLEMAAPYNTVLLNTFOEFFGLNCCSSNRDLQAMQVETLGTHTCCINPIIYAFV 300
QY 301 GERFRNLLVFPQKHIAKRCCKCSIFQDAPEPRASSVYTRSGEODISVGL 352
DB 301 GERFRNLLVFPQKHIAKRCCKCSIFQDAPEPRASSVYTRSGEODISVGL 352

RESULT 6
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; City: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-938-719-5

Query Match 100.0%; Score 1841; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYTSEPCQKINVKQIAARLLPPLYSIVETFGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINITYTSEPCQKINVKQIAARLLPPLYSIVETFGVGNMLVILLINCKR 60
QY 61 LKSMDDIYLLNLAISDLPELLTVPFAHAAAMOPGNTMOLLGLVPIGFSGIFFETI 120
DB 61 LKSMDDIYLLNLAISDLPELLTVPFAHAAAMOPGNTMOLLGLVPIGFSGIFFETI 120
QY 121 LTTIDRYLAVNAVAVALKARVTFGVVSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
DB 121 LTTIDRYLAVNAVAVALKARVTFGVVSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
QY 181 HEPYSQYOFWKNFQTLKIVILGLVPLVMVICYSGLTKTLRCRNEKKRRAVRLLIFTI 240
DB 181 HEPYSQYOFWKNFQTLKIVILGLVPLVMVICYSGLTKTLRCRNEKKRRAVRLLIFTI 240
QY 241 MIVYFLFAPRYNIVILLNTOEFPGIINNCSNRLDOAMQVETLGMTHCCINPIIYAV 300
DB 241 MIVYFLFAPRYNIVILLNTOEFPGIINNCSNRLDOAMQVETLGMTHCCINPIIYAV 300
QY 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGDEISVGL 352
DB 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGDEISVGL 352

RESULT 7

US-09-939-226-5
Sequence 5, Application US/09939226
Patent No. US20020110805A1

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knodde, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentia Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939,226

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-939-226-5

Query Match 100.0%; Score 1841; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYTSEPCQKINVKQIAARLLPPLYSIVETFGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINITYTSEPCQKINVKQIAARLLPPLYSIVETFGVGNMLVILLINCKR 60
QY 61 LKSMDDIYLLNLAISDLPELLTVPFAHAAAMOPGNTMOLLGLVPIGFSGIFFETI 120
DB 61 LKSMDDIYLLNLAISDLPELLTVPFAHAAAMOPGNTMOLLGLVPIGFSGIFFETI 120
QY 121 LTTIDRYLAVNAVAVALKARVTFGVVSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
DB 121 LTTIDRYLAVNAVAVALKARVTFGVVSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
QY 181 HEPYSQYOFWKNFQTLKIVILGLVPLVMVICYSGLTKTLRCRNEKKRRAVRLLIFTI 240
DB 181 HEPYSQYOFWKNFQTLKIVILGLVPLVMVICYSGLTKTLRCRNEKKRRAVRLLIFTI 240
QY 241 MIVYFLFAPRYNIVILLNTOEFPGIINNCSNRLDOAMQVETLGMTHCCINPIIYAV 300
DB 241 MIVYFLFAPRYNIVILLNTOEFPGIINNCSNRLDOAMQVETLGMTHCCINPIIYAV 300
QY 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGDEISVGL 352
DB 301 GEKFRNYLLVFPQKHIAKRFCKCSIFQOEAPERASSVYTRSTGDEISVGL 352

RESULT 8

US-09-938-703-5
Sequence 5, Application US/09938703
Patent No. US20020110870A1

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knodde, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentia Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:


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OY 121 LITIDRYLAHVAVFALKAARTVGVTSVITWVAVASLPGLITFSQKGLHYTSS 180
    |||
DB 121 LITIDRYLAHVAVFALKAARTVGVTSVITWVAVASLPGLITFSQKGLHYTSS 180
    |||
OY 181 HEPYSOYQWKNFQKLTIVIGLVPLVMVTCYSGLIKTLRCNEKKRRAVRLIFTI 240
    |||
DB 181 HEPYSOYQWKNFQKLTIVIGLVPLVMVTCYSGLIKTLRCNEKKRRAVRLIFTI 240
    |||
OY 241 MIYVFLFMAPIYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
    |||
DB 241 MIYVFLFMAPIYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
    |||
OY 301 GEKFRNYLLVFFQKHIAKRFCCSIFQOEAPERASSVYTRSTGEDEISVGL 352
    |||
DB 301 GEKFRNYLLVFFQKHIAKRFCCSIFQOEAPERASSVYTRSTGEDEISVGL 352
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RESULT 11

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US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2
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Query Match 99.6%; Score 1833; DB 9; Length 352;
Best Local Similarity 99.7%; Pred. No. 8.6e-150;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMLVILLINCKR 60
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DB 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMLVILLINCKR 60
    |||
OY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYAAQOMDFGNTMCOLLGLYFIFGFSGIFETI 120
    |||
DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYAAQOMDFGNTMCOLLGLYFIFGFSGIFETI 120
    |||
OY 121 LITIDRYLAHVAVFALKAARTVGVTSVITWVAVASLPGLITFSQKGLHYTSS 180
    |||
DB 121 LITIDRYLAHVAVFALKAARTVGVTSVITWVAVASLPGLITFSQKGLHYTSS 180
    |||
OY 181 HEPYSOYQWKNFQKLTIVIGLVPLVMVTCYSGLIKTLRCNEKKRRAVRLIFTI 240
    |||
DB 181 HEPYSOYQWKNFQKLTIVIGLVPLVMVTCYSGLIKTLRCNEKKRRAVRLIFTI 240
    |||
OY 241 MIYVFLFMAPIYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
    |||
DB 241 MIYVFLFMAPIYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
    |||
OY 301 GEKFRNYLLVFFQKHIAKRFCCSIFQOEAPERASSVYTRSTGEDEISVGL 352
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DB 301 GEKFRNYLLVFFQKHIAKRFCCSIFQOEAPERASSVYTRSTGEDEISVGL 352
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RESULT 12

US-09-725-285-2

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; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2
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Query Match 99.6%; Score 1833; DB 10; Length 352;
Best Local Similarity 99.7%; Pred. No. 8.6e-150;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMLVILLINCKR 60
    |||
DB 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMLVILLINCKR 60
    |||
OY 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYAAQOMDFGNTMCOLLGLYFIFGFSGIFETI 120
    |||
DB 61 LKSMTDIYLLNLAISDLFFLLTPFWAHYAAQOMDFGNTMCOLLGLYFIFGFSGIFETI 120
    |||
OY 121 LITIDRYLAHVAVFALKAARTVGVTSVITWVAVASLPGLITFSQKGLHYTSS 180
    |||
DB 121 LITIDRYLAHVAVFALKAARTVGVTSVITWVAVASLPGLITFSQKGLHYTSS 180
    |||
OY 181 HEPYSOYQWKNFQKLTIVIGLVPLVMVTCYSGLIKTLRCNEKKRRAVRLIFTI 240
    |||
DB 181 HEPYSOYQWKNFQKLTIVIGLVPLVMVTCYSGLIKTLRCNEKKRRAVRLIFTI 240
    |||
OY 241 MIYVFLFMAPIYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
    |||
DB 241 MIYVFLFMAPIYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
    |||
OY 301 GEKFRNYLLVFFQKHIAKRFCCSIFQOEAPERASSVYTRSTGEDEISVGL 352
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DB 301 GEKFRNYLLVFFQKHIAKRFCCSIFQOEAPERASSVYTRSTGEDEISVGL 352
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RESULT 13

```
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
```

PRIOR APPLICATION NUMBER: US 60/234,336
 PRIOR FILING DATE: 2000-09-22
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 22
 LENGTH: 352
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-779-879A-22

Query Match 99.6% Score 1833; DB 10; Length 352;
 Best Local Similarity 99.7% Pred. No. 8.6e-150;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMLVILLINCR 60
 DB 1 MDYVSSPIYDINITYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMLVILLINCR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLTPFPMAHYAAQMDFGNTKQLLGLYFIFGFGSIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFPMAHYAAQMDFGNTKQLLGLYFIFGFGSIFPII 120
 QY 121 LITDRYLAHVAVFALKARTVTCGVTSVITWVAVASLPGIIFTSQKGLHYTSS 180
 DB 121 LITDRYLAHVAVFALKARTVTCGVTSVITWVAVASLPGIIFTSQKGLHYTSS 180
 QY 181 HFPYSQYQFMKNFOTLKIIVILGLVPLLVWVICYSGLIKTLRCNKKRRRAVRLIFTI 240
 DB 181 HFPYSQYQFMKNFOTLKIIVILGLVPLLVWVICYSGLIKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIYVFLFAPYNIYLLNTFOEFGNLNCSNNRLDAQOYETELGMTHCCINPIYAFV 300
 DB 241 MIYVFLFAPYNIYLLNTFOEFGNLNCSNNRLDAQOYETELGMTHCCINPIYAFV 300
 QY 301 GEKFRNLYLVFFOKHIAKRFCKCSIFQOEAPEBASVYTTSTGEQISVGL 352
 DB 301 GEKFRNLYLVFFOKHIAKRFCKCSIFQOEAPEBASVYTTSTGEQISVGL 352

RESULT 14

US-09-779-880A-22
 Sequence 22, Application US/09779880A
 Patent No. US20020061834A1
 GENERAL INFORMATION:
 APPLICANT: Roschke, Craig A.
 APPLICANT: Roschke, Viktor
 APPLICANT: Li, Yi
 APPLICANT: Ruben, Steven, M.
 TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGKR10
 FILE REFERENCE: 1488.115000C
 CURRENT APPLICATION NUMBER: US/09/779, 880A
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/181,258
 PRIOR FILING DATE: 2000-02-09
 PRIOR APPLICATION NUMBER: US 60/187, 999
 PRIOR FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: US 60/234,336
 PRIOR FILING DATE: 2000-09-22
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 22
 LENGTH: 352
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-779-880A-22

Query Match 99.6% Score 1833; DB 10; Length 352;
 Best Local Similarity 99.7% Pred. No. 8.6e-150;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMLVILLINCR 60
 DB 1 MDYVSSPIYDINITYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMLVILLINCR 60

QY 61 LKSMTDIYLLNLAIISDLFFLLTPFPMAHYAAQMDFGNTKQLLGLYFIFGFGSIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFPMAHYAAQMDFGNTKQLLGLYFIFGFGSIFPII 120
 QY 121 LITDRYLAHVAVFALKARTVTCGVTSVITWVAVASLPGIIFTSQKGLHYTSS 180
 DB 121 LITDRYLAHVAVFALKARTVTCGVTSVITWVAVASLPGIIFTSQKGLHYTSS 180
 QY 181 HFPYSQYQFMKNFOTLKIIVILGLVPLLVWVICYSGLIKTLRCNKKRRRAVRLIFTI 240
 DB 181 HFPYSQYQFMKNFOTLKIIVILGLVPLLVWVICYSGLIKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIYVFLFAPYNIYLLNTFOEFGNLNCSNNRLDAQOYETELGMTHCCINPIYAFV 300
 DB 241 MIYVFLFAPYNIYLLNTFOEFGNLNCSNNRLDAQOYETELGMTHCCINPIYAFV 300
 QY 301 GEKFRNLYLVFFOKHIAKRFCKCSIFQOEAPEBASVYTTSTGEQISVGL 352
 DB 301 GEKFRNLYLVFFOKHIAKRFCKCSIFQOEAPEBASVYTTSTGEQISVGL 352

RESULT 15

US-09-195-662A-2
 Sequence 2, Application US/09195662A
 Patent No. US20020076745A1
 GENERAL INFORMATION:
 APPLICANT: Ruben, Steven, M.
 APPLICANT: Li, Yi
 TITLE OF INVENTION: Human G-protein Chemokine Receptor HDGKR10 (CCR5 Receptor)
 FILE REFERENCE: 1488.1150002
 CURRENT APPLICATION NUMBER: US/09/195, 662A
 CURRENT FILING DATE: 1998-11-18
 PRIOR APPLICATION NUMBER: 08/466,343
 PRIOR FILING DATE: 1995-06-06
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 LENGTH: 352
 TYPE: PRF
 ORGANISM: Artificial Sequence: Genomic
 FEATURE:
 OTHER INFORMATION: Deduced Amino Acid Sequence
 US-09-195-662A-2

Query Match 99.6% Score 1833; DB 10; Length 352;
 Best Local Similarity 99.7% Pred. No. 8.6e-150;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 1 MDYVSSPIYDINITYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMLVILLINCR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLTPFPMAHYAAQMDFGNTKQLLGLYFIFGFGSIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFPMAHYAAQMDFGNTKQLLGLYFIFGFGSIFPII 120
 QY 121 LITDRYLAHVAVFALKARTVTCGVTSVITWVAVASLPGIIFTSQKGLHYTSS 180
 DB 121 LITDRYLAHVAVFALKARTVTCGVTSVITWVAVASLPGIIFTSQKGLHYTSS 180
 QY 181 HFPYSQYQFMKNFOTLKIIVILGLVPLLVWVICYSGLIKTLRCNKKRRRAVRLIFTI 240
 DB 181 HFPYSQYQFMKNFOTLKIIVILGLVPLLVWVICYSGLIKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIYVFLFAPYNIYLLNTFOEFGNLNCSNNRLDAQOYETELGMTHCCINPIYAFV 300
 DB 241 MIYVFLFAPYNIYLLNTFOEFGNLNCSNNRLDAQOYETELGMTHCCINPIYAFV 300
 QY 301 GEKFRNLYLVFFOKHIAKRFCKCSIFQOEAPEBASVYTTSTGEQISVGL 352
 DB 301 GEKFRNLYLVFFOKHIAKRFCKCSIFQOEAPEBASVYTTSTGEQISVGL 352

Wed Jun 4 10:15:35 2003

Search completed: June 3, 2003, 15:34:30
Job time : 46.6279 secs

us-09-939-226-5.rapb

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2003, 15:21:53 ; Search time 22.3721 Seconds
(without alignments)
972.777 Million cell updates/sec

Title: US-09-939-226-6

Perfect score: 1122
Sequence: 1 MUYQVSSPIYDINYTSEPC.....AACGHLLGPNKNSASVK 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published, Applications, AA.*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1122	100.0	215	10	US-09-938-719-6 Sequence 6, Appl1
2	1122	100.0	215	10	US-09-939-226-6 Sequence 6, Appl1
3	1122	100.0	215	10	US-09-938-703-6 Sequence 6, Appl1
4	958	85.4	184	10	US-09-938-719-4 Sequence 4, Appl1
5	958	85.4	184	10	US-09-939-226-4 Sequence 4, Appl1
6	958	85.4	184	10	US-09-938-703-4 Sequence 4, Appl1
7	958	85.4	352	9	US-10-232-686-2 Sequence 2, Appl1
8	958	85.4	352	9	US-10-086-814-1 Sequence 1, Appl1
9	958	85.4	352	9	US-09-734-221A-14 Sequence 14, Appl1
10	958	85.4	352	10	US-09-725-285-2 Sequence 2, Appl1
11	958	85.4	352	10	US-09-759-841-2 Sequence 2, Appl1
12	958	85.4	352	10	US-09-779-880A-22 Sequence 22, Appl1
13	958	85.4	352	10	US-09-779-880A-22 Sequence 22, Appl1
14	958	85.4	352	10	US-09-813-653-15 Sequence 15, Appl1
15	958	85.4	352	10	US-09-796-202-1 Sequence 1, Appl1
16	958	85.4	352	10	US-09-195-662A-2 Sequence 2, Appl1
17	958	85.4	352	10	US-09-339-912A-2 Sequence 2, Appl1
18	958	85.4	352	10	US-09-938-719-5 Sequence 5, Appl1
19	958	85.4	352	10	US-09-939-226-5 Sequence 5, Appl1

20	958	85.4	352	10	US-09-938-703-5 Sequence 5, Appl1
21	958	85.4	352	10	US-09-502-783A-2 Sequence 2, Appl1
22	958	85.4	352	12	US-10-106-623-2 Sequence 2, Appl1
23	952	84.8	352	10	US-09-813-653-17 Sequence 17, Appl1
24	943	84.0	352	10	US-09-779-879A-2 Sequence 2, Appl1
25	943	84.0	352	10	US-09-779-880A-2 Sequence 2, Appl1
26	935	83.2	352	12	US-10-106-623-20 Sequence 20, Appl1
27	695	61.9	360	10	US-09-131-827A-20 Sequence 9, Appl1
28	694	61.9	344	9	US-10-232-686-9 Sequence 9, Appl1
29	694	61.9	344	10	US-09-779-879A-9 Sequence 9, Appl1
30	694	61.9	344	10	US-09-779-880A-9 Sequence 9, Appl1
31	694	61.9	347	10	US-09-104-792-3 Sequence 3, Appl1
32	694	61.9	360	10	US-09-131-827A-2 Sequence 3, Appl1
33	692	61.7	360	10	US-09-938-719-7 Sequence 7, Appl1
34	692	61.7	360	10	US-09-939-226-7 Sequence 7, Appl1
35	692	61.7	360	10	US-09-938-703-7 Sequence 7, Appl1
36	692	61.7	360	10	US-09-938-703-7 Sequence 7, Appl1
37	608.5	54.2	329	10	US-09-195-662A-9 Sequence 9, Appl1
38	608.5	54.2	329	10	US-09-339-912A-9 Sequence 9, Appl1
39	608.5	54.2	329	10	US-09-502-783A-9 Sequence 9, Appl1
40	598	53.3	355	10	US-09-961-068-1 Sequence 1, Appl1
41	598	53.3	355	10	US-09-960-547-1 Sequence 1, Appl1
42	598	53.3	375	9	US-10-219-834-78 Sequence 78, Appl1
43	594	52.9	385	10	US-09-938-719-9 Sequence 9, Appl1
44	594	52.9	385	10	US-09-939-226-9 Sequence 9, Appl1
45	594	52.9	385	10	US-09-938-703-9 Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-09-938-719-6
Sequence 6, Application US/09938719
Patent No. US20020106742A1

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARIENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
LIBERT, FREDERICK

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
City: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/09/938, 719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626, 939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-938-719-6

Query Match 100.0%; Score 1122; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2e-104;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFIFGVGNMVLILLINCKR 60
QY 61 LKSMTDIYLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOLLTGLYFIFGSGIFETI 120
DB 61 LKSMTDIYLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOLLTGLYFIFGSGIFETI 120
QY 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180
DB 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180
QY 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180
DB 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180
QY 181 HFPYIKDSHLGAGPAACHGHLLGNPKNSASVSK 215
DB 181 HFPYIKDSHLGAGPAACHGHLLGNPKNSASVSK 215

RESULT 2

US-09-939-226-6
Sequence 6, Application US/09939226
Patent No. US20020110805A1

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-939-226-6
Query Match 100.0%; Score 1122; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2e-104;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFIFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFIFGVGNMVLILLINCKR 60

DB 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFIFGVGNMVLILLINCKR 60

QY 61 LKSMTDIYLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOLLTGLYFIFGSGIFETI 120
DB 61 LKSMTDIYLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOLLTGLYFIFGSGIFETI 120
QY 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180
DB 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180
QY 181 HFPYIKDSHLGAGPAACHGHLLGNPKNSASVSK 215
DB 181 HFPYIKDSHLGAGPAACHGHLLGNPKNSASVSK 215

RESULT 3

US-09-938-703-6
Sequence 6, Application US/09938703
Patent No. US20020110870A1

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-938-703-6
Query Match 100.0%; Score 1122; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.2e-104;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFIFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFIFGVGNMVLILLINCKR 60
QY 61 LKSMTDIYLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOLLTGLYFIFGSGIFETI 120
DB 61 LKSMTDIYLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOLLTGLYFIFGSGIFETI 120
QY 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180
DB 121 LFTDRIYAAVHAVALKARTVFGVTVSVITWVAVFAASLPGLIFTRSQEGHLYTCSS 180

Db 121 LRTIDRYLAVVAVFLKARTVTEGVVTSYITWVAVFASLPGLITFRSOKEGLHYTCSS 180
QY 181 HFPYKDSHLGAGPAAACHGHLILGNPKNSASYK 215
Db 181 HFPYKDSHLGAGPAAACHGHLILGNPKNSASYK 215

RESULT 4
US-09-938-719-4

; Sequence 4, Application US/09938719
; Patent No. US20020106742A1

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

PARMENTIER, MARC

VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938, 719

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626, 939

FILING DATE: 27-JULY-2000

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-938-719-4

Query Match 85.4%; Score 958; DB 10; Length 184;

Best Local Similarity 100.0%; Pred. No. 7.5e-88;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDYOVSSPIYDINYTSEPCOKINVKQIAARLLPPLYSLVIFGFGNMLVILLINCKR 60

QY 61 LKSMTDIYLLNLAISDLFFLLTVPFNAHYAAQMDFGNTMCOLLTGLYFPGFSGIFFTI 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFNAHYAAQMDFGNTMCOLLTGLYFPGFSGIFFTI 120

QY 121 LRTIDRYLAVVAVFLKARTVTEGVVTSYITWVAVFASLPGLITFRSOKEGLHYTCSS 180
Db 121 LRTIDRYLAVVAVFLKARTVTEGVVTSYITWVAVFASLPGLITFRSOKEGLHYTCSS 180

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Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

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Db 181 HFPY 184

QY 181 HFPY 184
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QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

US-09-939-226-4
; Sequence 4, Application US/09939226
; Patent No. US20020110805A1

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

PARMENTIER, MARC

VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939, 226

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626, 939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-939-226-4

Query Match 85.4%; Score 958; DB 10; Length 184;

Best Local Similarity 100.0%; Pred. No. 7.5e-88;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYTSEPCOKINVKQIAARLLPPLYSLVIFGFGNMLVILLINCKR 60
Db 1 MDYOVSSPIYDINYTSEPCOKINVKQIAARLLPPLYSLVIFGFGNMLVILLINCKR 60

QY 61 LKSMTDIYLLNLAISDLFFLLTVPFNAHYAAQMDFGNTMCOLLTGLYFPGFSGIFFTI 120
Db 61 LKSMTDIYLLNLAISDLFFLLTVPFNAHYAAQMDFGNTMCOLLTGLYFPGFSGIFFTI 120

QY 121 LRTIDRYLAVVAVFLKARTVTEGVVTSYITWVAVFASLPGLITFRSOKEGLHYTCSS 180
Db 121 LRTIDRYLAVVAVFLKARTVTEGVVTSYITWVAVFASLPGLITFRSOKEGLHYTCSS 180

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

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Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
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QY 181 HFPY 184
Db 181 HFPY 184

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Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

QY 181 HFPY 184
Db 181 HFPY 184

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <unknown>

SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

Query Match
Best Local Similarity 100.0%; Pred. No. 7.5e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINNTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60

QY 61 LKSMDDIYLLNLAISDLFFLLTPFWAHYAAQMDFGNTMQLGLGYFIFGFGSIFPII 120
DB 61 LKSMDDIYLLNLAISDLFFLLTPFWAHYAAQMDFGNTMQLGLGYFIFGFGSIFPII 120

QY 121 LFTIDRYLAHVAVFALKARVTYFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
DB 121 LFTIDRYLAHVAVFALKARVTYFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180

QY 181 HFPY 184
DB 181 HFPY 184

RESULT 7
US-10-232-686-2
Sequence 2, Application US/10232686
Publication No. US20030023044A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-232-686-2

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINNTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60

QY 61 LKSMDDIYLLNLAISDLFFLLTPFWAHYAAQMDFGNTMQLGLGYFIFGFGSIFPII 120
DB 61 LKSMDDIYLLNLAISDLFFLLTPFWAHYAAQMDFGNTMQLGLGYFIFGFGSIFPII 120

QY 121 LFTIDRYLAHVAVFALKARVTYFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
DB 121 LFTIDRYLAHVAVFALKARVTYFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180

QY 181 HFPY 184
DB 181 HFPY 184

RESULT 8
US-10-086-814-1
Sequence 1, Application US/10086814
Publication No. US20030092632A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-086-814-1

Query Match
Best Local Similarity 85.4%; Score 958; DB 9; Length 352;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINNTYSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60

QY 61 LKSMDDIYLLNLAISDLFFLLTPFWAHYAAQMDFGNTMQLGLGYFIFGFGSIFPII 120
DB 61 LKSMDDIYLLNLAISDLFFLLTPFWAHYAAQMDFGNTMQLGLGYFIFGFGSIFPII 120

QY 121 LFTIDRYLAHVAVFALKARVTYFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
DB 121 LFTIDRYLAHVAVFALKARVTYFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180

QY 181 HFPY 184
DB 181 HFPY 184

RESULT 9
US-09-734-221A-14
Sequence 14, Application US/09734221A
Publication No. US20030096221A1

GENERAL INFORMATION:

APPLICANT: LITTMAN, DAN R.

DENG, HONGKUI

ELMEIER, WILFRIED

LANDAU, NATHANIEL R.

LIU, RONG

TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH

MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC

USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Software: Patent Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/734,221A

FILING DATE: 11-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/666,020

FILING DATE: 19-JUN-1996

APPLICATION NUMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 1049-1-004 N2

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-734-221A-14

Query Match 85.4% Score 958 DB 9 Length 352

Best Local Similarity 100.0% Pred. NO. 1.6e-87

Matches 184 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 MDYVSSPIYDINNTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVILLINCKR 60
DB 1 MDYVSSPIYDINNTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVILLINCKR 60
QY 61 LKSWTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLLTGLVFI GFSGIFETI 120
DB 61 LKSWTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLLTGLVFI GFSGIFETI 120
QY 121 LTTDRYLAHVHAFALKARTVTEGVTSVTWVAVFASLPGIIFRSOREGLHYTCSS 180
DB 121 LTTDRYLAHVHAFALKARTVTEGVTSVTWVAVFASLPGIIFRSOREGLHYTCSS 180
QY 181 HFPEY 184
DB 181 HFPEY 184

RESULT 10

US-09-725-285-2

Sequence 2, Application US/09725285

Patent No. US20010000241A1

GENERAL INFORMATION:

APPLICANT: LI, YI

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10

FILE REFERENCE: 1488,1150003

CURRENT APPLICATION NUMBER: US/09/725,285

CURRENT FILING DATE: 2000-11-29

PRIOR APPLICATION NUMBER: 09/339,912

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: 09/195,662

PRIOR FILING DATE: 1998-11-18

PRIOR APPLICATION NUMBER: 08/466,343

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patent version 3.0

SEQ ID NO 2

LENGTH: 352

TYPE: PRT

ORGANISM: Artificial Sequence: Genomic

FEATURE:

OTHER INFORMATION: Deduced Amino Acid Sequence

US-09-725-285-2

Query Match 85.4% Score 958 DB 10 Length 352
Best Local Similarity 100.0% Pred. NO. 1.6e-87
Matches 184 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 MDYVSSPIYDINNTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVILLINCKR 60
DB 1 MDYVSSPIYDINNTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVILLINCKR 60

QY 61 LKSWTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLLTGLVFI GFSGIFETI 120
DB 61 LKSWTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLLTGLVFI GFSGIFETI 120

QY 121 LTTDRYLAHVHAFALKARTVTEGVTSVTWVAVFASLPGIIFRSOREGLHYTCSS 180
DB 121 LTTDRYLAHVHAFALKARTVTEGVTSVTWVAVFASLPGIIFRSOREGLHYTCSS 180

QY 181 HFPEY 184
DB 181 HFPEY 184

RESULT 11

US-09-759-841-2

Sequence 2, Application US/09759841

Patent No. US20010039026A1

GENERAL INFORMATION:

APPLICANT: Rickelt, Graham A

APPLICANT: Dobbs, Susan

APPLICANT: Perros, Manousos

TITLE OF INVENTION: Assay Method

FILE REFERENCE: PC10348APME

CURRENT APPLICATION NUMBER: US/09/759,841

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: GB 0000661.9

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: GB 0000663.5

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: GB 0000659.3

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 2

LENGTH: 352

TYPE: PRT

ORGANISM: Homo sapiens

US-09-759-841-2

Query Match 85.4%; Score 958; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.6e-87; Indels 0; Gaps 0;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDYVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMVLILLINCKR 60
  |||||
DB 1 MDYVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMVLILLINCKR 60
QY 61 LKSMTDIYLNLAIISDLFEFLTFVPMWAAQAOMDFGNTMQLLTGLYIFGFSGIFPII 120
  |||||
DB 61 LKSMTDIYLNLAIISDLFEFLTFVPMWAAQAOMDFGNTMQLLTGLYIFGFSGIFPII 120
QY 121 LFTIDRYLAHVAVFALKARTVTEGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
  |||||
DB 121 LFTIDRYLAHVAVFALKARTVTEGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HEPY 184
  ||||
DB 181 HEPY 184
```

RESULT 12

US-09-779-879A-22

; Sequence 22, Application US/09779879A

; Patent No. US20020048786A1

; GENERAL INFORMATION:

; APPLICANT: Rosen, Craig A.

; APPLICANT: Roschke, Viktor

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

; FILE REFERENCE: 1488.115000A

; CURRENT APPLICATION NUMBER: US/09/779,879A

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,258

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: US 60/187,999

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/234,336

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-779-879A-22

Query Match 85.4%; Score 958; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.6e-87; Indels 0; Gaps 0;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDYVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMVLILLINCKR 60
  |||||
DB 1 MDYVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMVLILLINCKR 60
QY 61 LKSMTDIYLNLAIISDLFEFLTFVPMWAAQAOMDFGNTMQLLTGLYIFGFSGIFPII 120
  |||||
DB 61 LKSMTDIYLNLAIISDLFEFLTFVPMWAAQAOMDFGNTMQLLTGLYIFGFSGIFPII 120
QY 121 LFTIDRYLAHVAVFALKARTVTEGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
  |||||
DB 121 LFTIDRYLAHVAVFALKARTVTEGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HEPY 184
  ||||
DB 181 HEPY 184
```

RESULT 13

US-09-779-880A-22

; Sequence 22, Application US/09779880A

; Patent No. US20020061834A1

; GENERAL INFORMATION:

; APPLICANT: Rosen, Craig A.

; APPLICANT: Roschke, Viktor

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven, M.

; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

; FILE REFERENCE: 1488.115000C

; CURRENT APPLICATION NUMBER: US/09/779,880A

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,258

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: US 60/187,999

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/234,336

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-779-880A-22

Query Match 85.4%; Score 958; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.6e-87; Indels 0; Gaps 0;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDYVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMVLILLINCKR 60
  |||||
DB 1 MDYVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSLVTFEGVGNMVLILLINCKR 60
QY 61 LKSMTDIYLNLAIISDLFEFLTFVPMWAAQAOMDFGNTMQLLTGLYIFGFSGIFPII 120
  |||||
DB 61 LKSMTDIYLNLAIISDLFEFLTFVPMWAAQAOMDFGNTMQLLTGLYIFGFSGIFPII 120
QY 121 LFTIDRYLAHVAVFALKARTVTEGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
  |||||
DB 121 LFTIDRYLAHVAVFALKARTVTEGVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
QY 181 HEPY 184
  ||||
DB 181 HEPY 184
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RESULT 14

US-09-813-653-15

; Sequence 15, Application US/09813653

; Patent No. US20020064770A1

; GENERAL INFORMATION:

; APPLICANT: Nestor, John

; APPLICANT: Willson, Carol

; APPLICANT: See, Raymond

; APPLICANT: Tan Hehl, Christina

; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compound

; FILE REFERENCE: CNS-005

; CURRENT APPLICATION NUMBER: US/09/813,653

; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,946

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/190,996

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/191,299

; PRIOR FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-813-653-15

Query Match	85.48;	Score 958;	DB 10;	Length 352;
Best Local Similarity	100.0%;	Pred. No. 1.6e-87;		
Matches 184;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy

I MDYOVSSPIVDINNTSEPCOKINKQIAARLLPPLYSLVFIFGVGIMLVLILINCRR 60
|||||
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Dd

I MDYOVSSPIDINYTSEPCKIKNQIARRLLPPLSVLFIFGVGNMLVTILLINCRR 60
|||||

Qy 6 LKSMIDYLLNLAIISDLFLITLVPMPAHYAAQMDGNTMOLLTGTYFIFGFSGIFPII 120

Db 61 LKSMIDYLLNLAIISDLFLITLVPMPAHYAAQMDGNTMOLLTGTYFIFGFSGIFPII 120

Qy	Db
121	121
LLFTDRYLA	LLFTDRYLA
VAVH	VAVH
AVALKAT	AVALKAT
VTFC	VTFC
VTMT	VTMT
VWV	VWV
AV	AV
AS	AS
PGII	PGII
IF	IF
FR	FR
SQ	SQ
EG	EG
LH	LH
YCCS	YCCS
180	180
121	121
LLFTDRYLA	LLFTDRYLA
VAVH	VAVH
AVALKAT	AVALKAT
VTFC	VTFC
VTMT	VTMT
VWV	VWV
AV	AV
AS	AS
PGII	PGII
IF	IF
FR	FR
SQ	SQ
EG	EG
LH	LH
YCCS	YCCS
180	180

QY	181	HPY	184
Db	181	HPY	184

RESULT 15
US-09-796-202-1

Patent No. US20020068813A1

; GENERAL INFORMATION:

APPLICANT: Dragica, Tatjana

APPLICANT: OLSON, William

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CURRENT APPLICATION NUMBER: US/09/796, 202

; CURRENT FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 17

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; SOFTWARE: PatentIn version 3.0
; GEO TO NO 1

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LENGTH: 352
TYPE: PPT

TYPE: PRT
ORGANISM: h

ORGANISM: *h*
US-09-796-202-1

T-707-96/-60-50

Query Match

Query Match	85.40;	Score	958;	DB	10;	Length	352;
Best Local Similarity	100.00;	Pred. NO.	1.6e-87;				
Matches	184;	Conservative	0;	Mismatches	0;	Indels	0;
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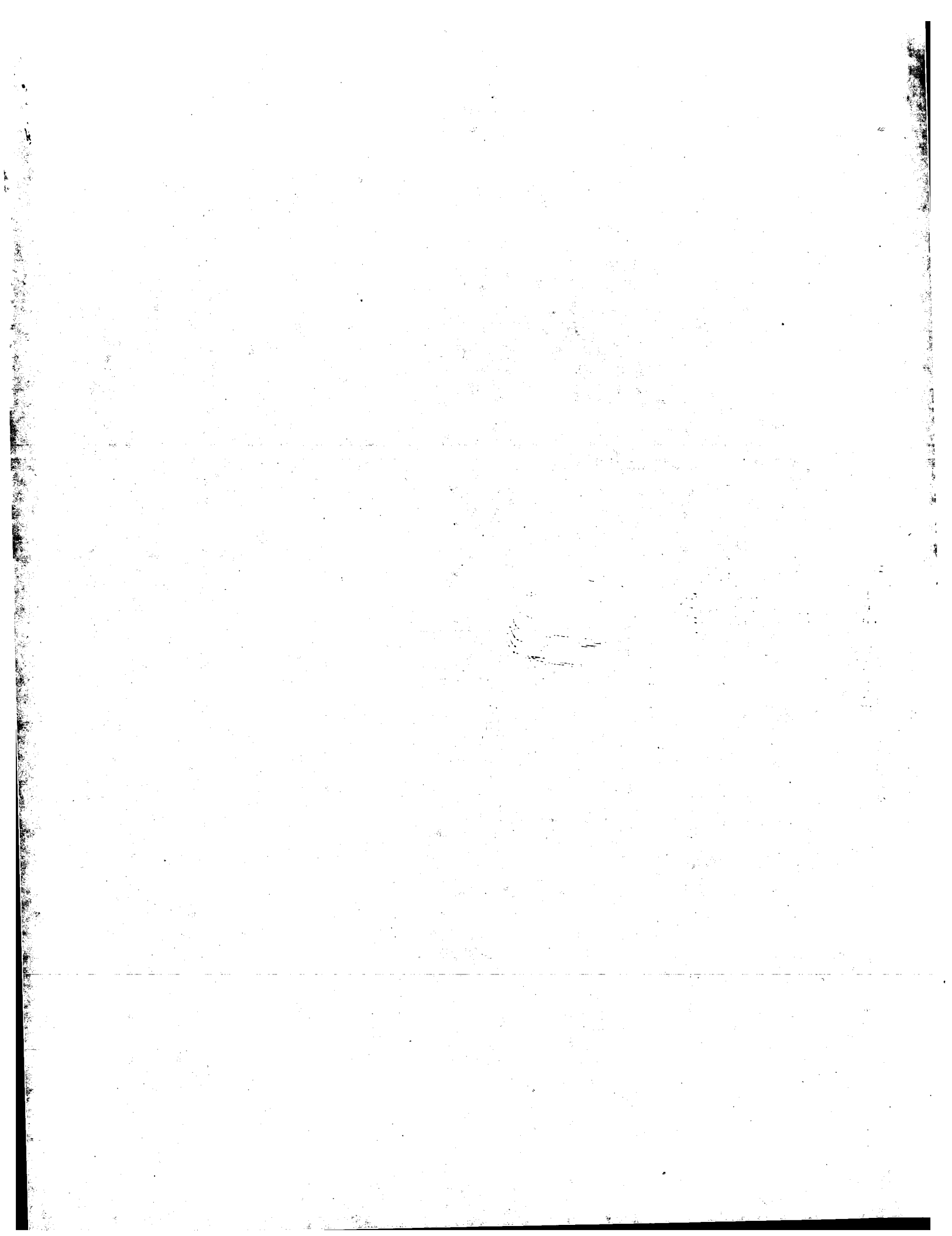
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Db 1 MDYGVSSPIVDINYYTSEPCOKINQVIAARLLPPLYSLVETFEFGVGNLVILINCKR 60

Qy 61 LKSMIDYLYLNLAIASDLEFLLTVPFAAHYAAQWDCGNTMKOLLTGIFYIFGFSGIFPII 120Q
Db 61 LKSMIDYLYLNLAIASDLEFLLTVPFAAHYAAQWDCGNTMKOLLTGIFYIFGFSGIFPII 120Q

Oy	121	LTTIDRYLAVVHAVALKARVTGCVTSVTTWVAVFASLPGLIFPRSOKEELHYTCSS	180Q
Db	121	LTTIDRYLAVVHAVALKARVTGCVTSVTTWVAVFASLPGLIFPRSOKEELHYTCSS	180Q

OY	181	HPY	184
		1111	
Db	181	HPY	184

Search completed: June 3, 2003, 15:34:30
Job time : 22.3721 sec



GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 3, 2003, 15:09:10 ; Search time 39.4356 Seconds (without alignments)

(without alignments)
726.472 Million cell updates/sec

Title: US-09-939-226-6

Perfect score: 1122
Sequence: 1 MDQVSSPIVDINTYSEPC.....AACHGILLGNPKNSASVSK 215

Scoring table: BLOSUM62
GapPen 10.0, GapExt 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1122	100.0	215	18	AAW27408	Inactive human CCR
2	1122	100.0	215	20	AAW88238	HIV-1 co-receptor
3	958	85.4	184	18	AAW27406	Inactive human CCR
4	958	85.4	352	18	AAW27407	Human CCR5. Homo
5	958	85.4	352	18	AAW27123	Human chemokine re
6	958	85.4	352	19	AAW23835	Human CC chemokine
7	958	85.4	352	20	AAW88232	HIV-1 co-receptor
8	958	85.4	352	22	ABW56342	Non-endogenous hum
9	958	85.4	352	22	ANG80111	Human CCR5 protein
10	958	85.4	352	22	AAW82948	Human HIV-1 co-rec

11	958	85.4	352	22	AAE07039	Human G-protein ch
12	958	85.4	352	22	AAE07048	Human G-protein ch
13	958	85.4	352	22	AAE83354	Human CCR5 protein
14	958	85.4	352	22	AAE04371	Human chemokine re
15	958	85.4	352	22	AAE86858	Human HDXNR10 prot
16	958	85.4	352	23	AAU57152	Human G-protein ch
17	958	85.4	352	23	AAE08343	Human chemokine (C
18	958	85.4	352	23	AAE52828	Human CC chemokine
19	958	85.4	439	20	AAE41280	Fusion protein con
20	952	84.9	371	19	AAE23894	Human CC chemokine
21	952	84.8	352	23	AAE52829	Human CCR5 Gln 55
22	943	84.0	352	18	AAE07602	Human G-protein ch
23	943	84.0	352	21	AAE80128	Human G-protein ch
24	943	84.0	352	22	AAE07037	Human G-protein ch
25	943	84.0	352	22	AAE07046	Human G-protein ch
26	943	84.0	352	23	AAU57150	Human G-protein ch
27	936	83.4	352	22	AAE79089	Amino acid sequenc
28	933	83.2	352	18	AAE27125	Macaque chemokine
29	839	74.8	332	18	AAE26756	Human chemokine re
30	776	69.2	354	19	AAE54037	Mouse CC-CR5 prot
31	695	61.9	360	22	AAU07613	Human CCR2-641 pol
32	694	61.9	360	16	AAE79166	Human monocyte che
33	694	61.9	360	18	AAE58833	Human monocyte che
34	694	61.9	360	22	AAE56340	Non-endogenous hum
35	694	61.9	360	22	AAE80108	Human CCR2b protei
36	694	61.9	360	22	AAU07614	Human wild-type CCR
37	694	61.9	374	16	AAE79165	Human monocyte che
38	694	61.9	374	16	AAE80107	Human CCR2a protei
39	608.5	54.2	329	22	AAE86859	Human MCP-1 recep
40	598	53.3	355	15	AAE52749	C-C chemokine rece
41	598	53.3	355	18	AAE26581	Human MIP-1 alpha/
42	598	53.3	355	18	AAE25751	Human MIP-1alpha/B
43	598	53.3	355	21	AAE20571	Human CC-chemokine
44	565.5	50.4	355	18	AAE28179	Rat CC chemokine r
45	547.5	48.8	360	17	AAE9274	Chemokine receptor

ALIGNMENTS

XX	AAW27408	standard; Proteoln; 215 AA.
XX	AAW27408;	
XX	14-APR-1998	(first entry)
XX	Inactive human CCR5.	
XX	Inactive; human Cys-Cys chemokine receptor 5; CCR5;	
KW	human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;	
KW	predisposition; resistance; diagnosis; treatment; prevention;	
KW	inflammatory disease; rheumatoid arthritis; glomerulonephritis;	
KW	asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;	
KW	cancer; atherosclerosis; autoimmune disorder.	
XX	Homo sapiens.	
XX	W09732019-A2.	
XX	04-SEP-1997.	
XX	28-FEB-1997;	97MO-BE00023.
XX	06-AUG-1996;	96EP-0870102.
XX	01-MAR-1996;	96EP-0870021.
XX	(EURO-) EUROSCREEN SA.	
PI	Libert F, Parmentier M, Samson M, Vassart G;	
XX	WPI; 1997-479829/44.	

DR N-PSDB; AAM790118.

PT Active and inactive forms of human CC chemokine receptor CCR-5
PT useful to diagnose, prevent and/or treat inflammatory disorders,
PT autoimmune disease and viral infection

PS Claim 7, Fig 1d-e; 94pp; English.

CC The present sequence is an inactive human CC (Cys-Cys)
CC chemokine receptor 5 (CCR5), which lacks the last 3 transmembrane
CC regions and the regions involved in G protein-coupling. CCR5 or
CC its cDNA can be used to diagnose, treat and/or prevent inflammatory
CC diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma,
CC idiopathic pulmonary fibrosis and psoriasis, viral infections,
CC especially human immunodeficiency virus type 1 or type 2 (HIV-1 or
CC HIV-2) infection, cancer, atherosclerosis and autoimmune disorders.
CC Subjects that express the inactive receptor have a predisposition,
CC or resistance to HIV-1 and/or HIV-2.

CC Sequence 215 AA;

Query Match 100.0%; Score 1122; DB 18; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPPLYSVIFGFYGNMVLILLNCR 60
DB 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPPLYSVIFGFYGNMVLILLNCR 60
QY 61 LKSMIDYVLLNLAISDLFFLLVPPWAHAAQMDGNTMCLLGLYFIFGFSGIFFTI 120
DB 61 LKSMIDYVLLNLAISDLFFLLVPPWAHAAQMDGNTMCLLGLYFIFGFSGIFFTI 120
QY 121 LITIDRYLAHVAVFALKAFTVFGVTSVITWVAVFASLPGLIFTSQKGLHYTCSS 180
DB 121 LITIDRYLAHVAVFALKAFTVFGVTSVITWVAVFASLPGLIFTSQKGLHYTCSS 180
QY 181 HPPYIKDSHLGAGPAAACHGILLGNPKNSASVSK 215
DB 181 HPPYIKDSHLGAGPAAACHGILLGNPKNSASVSK 215

RESULT 2
AAM8238
ID AAM8238 standard; Protein: 215 AA.

AC AAM8238;

DT 15-MAR-1999 (first entry)

DE HIV-1 co-receptor CCR5 variant CCR5-delta32.

KW HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;

KW gene therapy; human.

OS Homo sapiens.

Key Location/Qualifiers
Domain 32..56 /note= "transmembrane domain 1"
Domain 67..87 /note= "transmembrane domain 2"
Domain 103..124 /note= "transmembrane domain 3"
Domain 142..167 /note= "transmembrane domain 4"

MO9854317-A1.
03-DEC-1998.
29-MAY-1998; 98WO-EP03437.

PR 30-MAY-1997; 97US-0048057.

PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

PI Arenzana Siesdedos F, Beretta A, Braun J, Quillent C;

DR WPI; 1999-059835/05.

DR N-PSDB; AAM84159.

PT New CCR5 variant protein of the HIV-1 co-receptor - useful in
PT developing resistance of CCR5-expressing cells to HIV-1 infection
PS Disclosure; Page 38-39; 55pp; English.

CC This is the amino acid sequence of a CCR5 variant protein,
CC designated CCR5-delta32, that includes the first 4 transmembrane
CC domains of wild-type CCR5 (see AAM8232), but lacks transmembrane
CC domains 5-7. CCR5 serves as a co-receptor for infection by
CC macrophage-tropic (M-tropic) strains of HIV-1. Individuals
CC homozygous for the CCR5-delta32 mutation are resistant to HIV-1
CC infection, but heterozygous individuals are susceptible. The
CC invention additionally relates to the identification of variant
CC CCR5s (see AAM8231), which lack transmembrane domains 3-7 of
CC CCR5. The detection of CCR5 variants may be used to identify
CC individuals at lower risk of infection relative to the general
CC population who, if infected, may exhibit slower progression to
CC AIDS. Probes and primers (see AAM84127-36) are provided for use in
CC diagnostic methods for detecting the presence of such variants. A
CC method is provided for inhibiting HIV-1 infection of a cell
CC expressing the CCR5 receptor. This involves introducing a nucleic
CC acid encoding a CCR5 variant into the cell, thereby reducing the
CC number of functional CCR5 molecules present on the cell surface.

QY Sequence 215 AA;
Query Match 100.0%; Score 1122; DB 20; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPPLYSVIFGFYGNMVLILLNCR 60
DB 1 MDYVSSPIYDINVTYSEPCQKINVKQIARLLPPLYSVIFGFYGNMVLILLNCR 60
QY 61 LKSMIDYVLLNLAISDLFFLLVPPWAHAAQMDGNTMCLLGLYFIFGFSGIFFTI 120
DB 61 LKSMIDYVLLNLAISDLFFLLVPPWAHAAQMDGNTMCLLGLYFIFGFSGIFFTI 120
QY 121 LITIDRYLAHVAVFALKAFTVFGVTSVITWVAVFASLPGLIFTSQKGLHYTCSS 180
DB 121 LITIDRYLAHVAVFALKAFTVFGVTSVITWVAVFASLPGLIFTSQKGLHYTCSS 180
QY 181 HPPYIKDSHLGAGPAAACHGILLGNPKNSASVSK 215
DB 181 HPPYIKDSHLGAGPAAACHGILLGNPKNSASVSK 215

RESULT 3
AAM27406
ID AAM27406 standard; Protein: 184 AA.

AC AAM27406;

DT 14-APR-1998 (first entry)

DE Inactive human CCR5.

KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;
KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
KW predisposition; resistance; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
KW cancer; atherosclerosis; autoimmune disorder.

OS Homo sapiens.
 XX MO9732019-A2.
 XX 04-SEP-1997.
 XX 28-FEB-1997; 97WO-BE00023.
 XX 06-AUG-1996; 96EP-0870102.
 PR 01-MAR-1996; 96EP-0870021.
 XX (EURO-) EUROSREEN SA.
 PA Libert F, Parmentier M, Samson M, Vassart G;
 PI WPI: 1997-479829/44.
 DR N-PSDB; AAT90116.
 XX
 PT Active and inactive forms of human CC chemokine receptor CCR-5 -
 PT useful to diagnose, prevent and/or treat inflammatory disorders,
 PT autoimmune disease and viral infection
 XX
 PS Claim 1: Fig 1a; 94pp; English.
 CC The present sequence is an inactive human CC (Cys-Cys)
 CC chemokine receptor 5 (CCR5), which is not a receptor of human
 CC immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or
 CC its cDNA can be used to diagnose, treat and/or prevent inflammatory
 CC diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma,
 CC idiopathic pulmonary fibrosis and psoriasis, viral infections,
 CC especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and
 CC autoimmune disorders. Subjects that express the inactive receptor
 CC have a predisposition, or resistance to HIV-1 and/or HIV-2.
 XX
 SQ Sequence 184 AA;
 Query Match 85.4%; Score 958; DB 18; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4,4e-106; Indels 0; Gaps 0;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVFIFGFGNMLVILLINCKR 60
 Db 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVFIFGFGNMLVILLINCKR 60
 Oy 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOLLTGLYIFGFGSGIFPII 120
 Db 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOLLTGLYIFGFGSGIFPII 120
 Oy 121 LRTDRYLAIVVHAFALKARTVFGVTSVITWVAVFASLPGLIFTRSORKEGLHYTCSS 180
 Db 121 LRTDRYLAIVVHAFALKARTVFGVTSVITWVAVFASLPGLIFTRSORKEGLHYTCSS 180
 Oy 181 HFPY 184
 Db 181 HFPY 184
 RESULT 4
 AAM27407 standard; Protein: 352 AA.
 AC AAM27407;
 DT 14-APR-1998 (first entry)
 DE Human CCR5.
 KW Human Cys-Cys chemokine receptor 5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
 KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
 KW cancer; atherosclerosis; autoimmune disorder.

XX Homo sapiens.
 OS MO9732019-A2.
 XX 04-SEP-1997.
 XX 28-FEB-1997; 97WO-BE00023.
 XX 06-AUG-1996; 96EP-0870102.
 PR 01-MAR-1996; 96EP-0870021.
 XX (EURO-) EUROSREEN SA.
 PA Libert F, Parmentier M, Samson M, Vassart G;
 PI WPI: 1997-479829/44.
 DR N-PSDB; AAT90117.
 XX
 PT Active and inactive forms of human CC chemokine receptor CCR-5 -
 PT useful to diagnose, prevent and/or treat inflammatory disorders,
 PT autoimmune disease and viral infection
 XX
 PS Claim 4: Fig 1b-c; 94pp; English.
 CC The present sequence is human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES
 CC chemokines, but not by monocyte chemoattractant protein 1 (MCP-1).
 CC MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product
 CC alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of
 CC human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2).
 CC CCR5 or its cDNA can be used to diagnose, treat and/or prevent
 CC inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection,
 CC cancer, atherosclerosis and autoimmune disorders.
 XX
 SQ Sequence 352 AA;
 Query Match 85.4%; Score 958; DB 18; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-105;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVFIFGFGNMLVILLINCKR 60
 Db 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVFIFGFGNMLVILLINCKR 60
 Oy 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOLLTGLYIFGFGSGIFPII 120
 Db 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOLLTGLYIFGFGSGIFPII 120
 Oy 121 LRTDRYLAIVVHAFALKARTVFGVTSVITWVAVFASLPGLIFTRSORKEGLHYTCSS 180
 Db 121 LRTDRYLAIVVHAFALKARTVFGVTSVITWVAVFASLPGLIFTRSORKEGLHYTCSS 180
 Oy 181 HFPY 184
 Db 181 HFPY 184
 RESULT 5
 AAM27123 standard; Protein: 352 AA.
 AC AAM27123;
 DT 14-DEC-1997 (first entry)
 DE Human chemokine receptor 88C.
 KW Human chemokine receptor 88C;
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;

KW G protein coupled receptor; ligand; modulator; antibody; human.
 XX Homo sapiens.

FT Key Location/Qualifiers
 FT Domain 1..32
 FT /label= Extracellular_domain
 FT Domain 56..67
 FT /label= Intracellular_domain
 FT Domain 89..112
 FT /label= Extracellular_domain
 FT Domain 125..145
 FT /label= Intracellular_domain
 FT Domain 166..191
 FT /label= Extracellular_domain
 FT Domain 213..235
 FT /label= Intracellular_domain
 FT Domain 259..280
 FT /label= Extracellular_domain
 FT Domain 301..352
 FT /label= Intracellular_domain

PN W09722698-A2.
 XX 26-JUN-1997.
 PD 20-DEC-1996; 96WO-US20759.
 XX 07-JUN-1996; 96US-0661393.
 PR 20-DEC-1995; 95US-0575967.
 XX (ICOS-) ICOS CORP.

PI Gray PW, Raport CJ, Schweickart VL;
 DR WPI; 1997-341689/31.
 DR N-PSDB; AAT85161.

XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used
 PT to modulate leukocyte trafficking, e.g. for treatment of
 FT inflammation, tumours, viral infections, autoimmune diseases, etc.

XX Claim 16; Page 47-48; 65pp; English.

XX This polypeptide sequence comprises novel human chemokine receptor
 CC 88C, a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a cDNA clone
 CC (AAT85161) isolated from a macrophage library. It shows 62% identity
 CC to CCRK1. Chemokine receptor 88-2B (see AAW27124) has also been
 CC identified. 88C and 88-2B receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides
 CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc.

XX Sequence 352 AA;

Query Match 85.4%; Score 958; DB 18; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-105;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIYDINYSSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLNCKR 60
 DB 1 MDYQVSSPIYDINYSSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLNCKR 60
 QY 61 LKSMTDIYLLNLASIDLPFLITVPFAHAYAAQWDGNTMCCOLLTGIFGFGSGIFPII 120
 DB 61 LKSMTDIYLLNLASIDLPFLITVPFAHAYAAQWDGNTMCCOLLTGIFGFGSGIFPII 120

QY 121 LITIDRYLAVYHVAFAKARTVFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
 DB 121 LITIDRYLAVYHVAFAKARTVFGVTVSVITWVAVFASLPGLIFTRSQKEGLHYTCSS 180
 QY 181 HFPY 184
 DB 181 HFPY 184

RESULT 6
 AAW23835 standard; Protein; 352 AA.
 ID AAW23835
 AC AAW23835;
 XX 08-JUN-1998 (first entry)

DE Human CC chemokine receptor 5 (CCR5).

KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
 KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;
 KW transgenic animal.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 29..55
 FT /label= I
 FT /note= "transmembrane domain"

FT Region 109..120
 FT /note= "extracellular loop-1 (Claim 19)"

FT Domain 104..126
 FT /label= III
 FT /note= "transmembrane domain"

FT Domain 143..171
 FT /label= IV
 FT /note= "transmembrane domain"

FT Region 187..210
 FT /note= "extracellular loop-2 (Claim 19)"

FT Domain 194..219
 FT /label= V
 FT /note= "transmembrane domain"

FT Domain 238..258
 FT /label= VI
 FT /note= "transmembrane domain"

FT Region 261..276
 FT /note= "extracellular loop-3 (Claim 19)"

FT Domain 277..300
 FT /label= VII
 FT /note= "transmembrane domain"

W09745543-A2.

04-DEC-1997.

28-MAY-1997; 97WO-US09586.

28-MAY-1996; 96US-0018508.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Alkhatib G, Berger EA, Broder CC, Combadiere C;
 Feng Y, Kennedy PE, Murphy PM;

WPI; 1998-032650/03.
 N-PSDB; AAT76920.

CC chemokine receptor 5 polypeptide - used to inhibit membrane
 fusion between HIV and a target cell

Claim 68; Fig 1C; 70pp; English.

This protein sequence comprises of a novel human macrophage-selective

T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
anaphylaxis; malignancy; inflammation; histamine; IGE; silicosis; shock;
immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
Klebsiella pneumoniae-independent fever; bone marrow failure; sarcoidosis;
hyper-eosinophilic syndrome; vulvovaginitis;
Homo sapiens.
US2001000241-A1.
12-APR-2001.
29-NOV-2000; 2000US-0725285.
06-JUN-1995; 95US-0466343.
18-NOV-1998; 98US-0195662.
25-JUN-1999; 99US-0339912.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
LI Y, Ruben SM;
WPI; 2001-226317/23.
N-PSDB; AAF26390.

New human G-protein chemokine receptor polypeptides and
polynucleotides, useful for identifying (ant)agonists to the G-protein
chemokine receptor .

Claim 1a; Page 15; 22pp; English.

This invention describes a novel receptor polypeptide (I) selected from
(i) a fully defined 329 amino acid sequence (II) fully disclosed in the
specification; and (ii) a polypeptide encoded by the cDNA contained in a
plasmid, and fragments, analogs and derivatives of the polypeptide. The
products of the invention have anti-inflammatory, immunomodulatory,
anticoagulant, antiallergic, immunosuppressive, vulvovaginitis, cytostatic,
antiparasitic, antipsoriatic, antirheumatic, antiallergic and vasotropic
activity and can be used for gene therapy. The G-protein chemokine
receptor, HDGKR10, (I) are useful for screening for compounds which
activate or inhibit activation of (I). The products of the invention can
also be used for stimulating hematopoiesis, wound healing, coagulation,
angiogenesis, treating solid tumours, chronic infections, leukemia,
T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and
stimulating growth factor activity. HDGKR10 is useful for treating
allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
reactions, prostaglandin-independent fever, bone marrow failure,
silicosis, sarcoidosis, rheumatoid arthritis, shock and
hyper-eosinophilic syndrome.
(N.B. This record was resubmitted to correct errors in the keyword
formatting).

Sequence 352 AA;

Query Match 85.4%; Score 958; DB 22; Length 352;

Best Local Similarity 100.0%; Pred. No. 1e-105;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVFIPIFGVGMVILILINCKR 60
DB 1 MDYVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVFIPIFGVGMVILILINCKR 60
QY 61 LKSTFDIYLNLASDLEFLITVPFAHYAAQWDFGNTMCQLLTGLYIFGFSGIFETI 120
DB 61 LKSTFDIYLNLASDLEFLITVPFAHYAAQWDFGNTMCQLLTGLYIFGFSGIFETI 120
QY 121 LKSTFDIYLNLASDLEFLITVPFAHYAAQWDFGNTMCQLLTGLYIFGFSGIFETI 180
DB 121 LKSTFDIYLNLASDLEFLITVPFAHYAAQWDFGNTMCQLLTGLYIFGFSGIFETI 180
QY 181 HFPY 184

DB 181 HFPY 184

Search completed: June 3, 2003, 15:19:03
Job time : 40.4356 secs

SO Sequence 352 AA;

Query Match 85.4%; Score 958; DB 22; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-105;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINVTYSEPCOKINVKQIAARLLPPLYSLVFIFGVGMNLVILINCKR 60
 DB 1 MDYOVSSPIYDINVTYSEPCOKINVKQIAARLLPPLYSLVFIFGVGMNLVILINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDGNTMCOLLTGLYFGFSGIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDGNTMCOLLTGLYFGFSGIFPII 120
 QY 121 LTTIDRYLAVVAVFALKARTVTGVTYVITWVAVASLPGIIFTRSQEGSLHYTCSS 180
 DB 121 LTTIDRYLAVVAVFALKARTVTGVTYVITWVAVASLPGIIFTRSQEGSLHYTCSS 180
 QY 181 HFPY 184
 DB 181 HFPY 184

RESULT 12
 AAE07048
 ID AAE07048 standard; Protein; 352 AA.
 AC AAE07048;
 XX
 DT 16-OCY-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; valine; therapy;
 KW cytoskeletal; immunosuppressive; nocturnal; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 PN
 PN W0200158916-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001MO-US04153.
 XX
 PR 09-FEB-2000; 2000US-0181258.
 PR 09-MAR-2000; 2000US-0187999.
 PR 22-SEP-2000; 2000US-0234336.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 DR WPI: 2001-488966/53.
 DR N-PSDB; AAD13299.
 XX
 PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating
 PT autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 PT disorders and neurodegenerative disorders -
 XX
 PS Example 40; Page 504-505; 518pp; English.
 CC
 CC The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies
 CC are useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune

CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemia) and
 CC wound healing. The present sequence is human CCR5 HDGNR10 protein.

SO Sequence 352 AA;

Query Match 85.4%; Score 958; DB 22; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-105;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINVTYSEPCOKINVKQIAARLLPPLYSLVFIFGVGMNLVILINCKR 60
 DB 1 MDYOVSSPIYDINVTYSEPCOKINVKQIAARLLPPLYSLVFIFGVGMNLVILINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDGNTMCOLLTGLYFGFSGIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDGNTMCOLLTGLYFGFSGIFPII 120
 QY 121 LTTIDRYLAVVAVFALKARTVTGVTYVITWVAVASLPGIIFTRSQEGSLHYTCSS 180
 DB 121 LTTIDRYLAVVAVFALKARTVTGVTYVITWVAVASLPGIIFTRSQEGSLHYTCSS 180
 QY 181 HFPY 184
 DB 181 HFPY 184

RESULT 13

ID AAB83354 standard; Protein; 352 AA.

AC AAB83354;
 XX
 DT 09-OCY-2001 (first entry)
 XX
 DE Human CCR5 protein sequence.
 XX
 KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KW human immunodeficiency virus; anti-inflammatory disease; human.
 XX
 OS Homo sapiens.
 PN
 PN EP1118858-A2.
 XX
 PD 25-JUL-2001.
 XX
 PF 03-JAN-2001; 2001EP-0300020.
 PR 12-JAN-2000; 2000GB-0000659.
 PR 12-JAN-2000; 2000GB-0000661.
 PR 12-JAN-2000; 2000GB-0000663.
 XX
 PA (Pfizer) Pfizer Ltd.
 PA (Pfizer) Pfizer Inc.
 PI Dobbs S, Petros M, Rickett GA;
 XX

Query Match	Best Local Similarity	Matches 184;	Conservative	Score 958;	DB 22;	Length 352;
	100.0%;	0;	Mismatches	0;	Indels	Gaps
0Y	1	MDYOVSSPIVDINTYTSSEPCOKINVKQIARLLPLIXSVITFTGFVGNLVLILINCKR	60			
Db	1	MDYOVSSPIVDINTYTSSEPCOKINVKQIARLLPLIXSVITFTGFVGNLVLILINCKR	60			
0Y	61	LKSWTDIYILNIAISDFLLITVPFMAHYAAAMDGNTWCQDITGLYPIGFSGIFITII	120			
Db	61	LKSWTDIYILNIAISDFLLITVPFMAHYAAAMDGNTWCQDITGLYPIGFSGIFITII	120			
0Y	121	LLTIDRYLAVHVAFAFKARTVTFGVTSYITWVAVFASLPGLIFTRSKBEIAHTCSS	180			
Db	121	LLTIDRYLAVHVAFAFKARTVTFGVTSYITWVAVFASLPGLIFTRSKBEIAHTCSS	180			
0Y	181	HPFY 184				

Db	181 HEPY 184
XX	RESULT 11
XX	AAE07039
XX	AAE07039 standard; Protein: 352 AA.
XX	AAE07039;
XX	16-OCT-2001 (first entry)
XX	
XX	Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX	
XX	Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
XX	human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
XX	cytotoxic; immunosuppressive; neoplastic; neuroprotective; gene therapy;
XX	neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
XX	rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
XX	gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
XX	haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
XX	multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
XX	cardiovascular disorder; myocardial ischaemia.
XX	
XX	Homo sapiens.
XX	
XX	WO200158915-A2.
XX	16-AUG-2001.
XX	09-FEB-2001; 2001MO-US04152.
XX	
XX	09-FEB-2000; 2000US-0181258.
XX	09-MAR-2000; 2000US-0187999.
XX	22-SEP-2000; 2000US-0234336.
XX	
XX	(HUMA-) HUMAN GENOME SCI INC.
XX	
XX	Rosen CA, Roschke V, Li Y, Ruben SM;
XX	
XX	WPI; 2001-488965/53.
XX	N-PSDB; AAD13198.
XX	
XX	Isolated nucleic acid encoding a human G-protein chemokine receptor
XX	(CCR5) HDGNR10 polypeptide, useful for preventing or treating
XX	autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX	disorders and neurodegenerative disorders -
XX	
XX	Example 40; Page 486-487; 495pp; English.
XX	
XX	The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
XX	protein. CCR5 HDGNR10 antibodies are useful for treating, preventing
XX	or ameliorating a disease or disorder associated with inflammation,
XX	defective or aberrant chemotaxis of immune cells, HIV infection (such as
XX	Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
XX	aberrant T-cell antigen presenting cell interaction. The disease or
XX	disorder may also be an infectious disease (e.g. a viral infection such
XX	as an early stage HIV infection, a cytomegalovirus infection, or a
XX	poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
XX	a neurodegenerative disorder. The disease or disorder may be associated
XX	with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
XX	ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
XX	is used as a food additive or preservative to increase or decrease
XX	storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
XX	identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
XX	antibodies, agonists and antagonists are also useful in the
XX	diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
XX	gland, bone, bone marrow, gastrointestinal tract, liver, lung,
XX	urogenital); immune disorders (Addison's disease, allergies, autoimmune
XX	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX	disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX	colitis); cardiovascular disorders (myocardial ischaemias) and
XX	wound healing.
XX	

OS	Homo sapiens.
XX	
PN	W0200172830-A2.
XX	
PD	04-OCT-2001.
XX	
XX	02-APR-2001; 2001WO-EP03708.
PF	
PR	31-MAR-2000; 2000DE-1016013.
XX	
PA	(IPPE-) IPF PHARM GMBH.
XX	(FORS/) FORSMANN U.
PI	Forsmann W, Adermann K, Heitland A, Spodberg N;
DR	WPL; 2001-626256/72.
XX	
PT	Diagnostic agent containing two or more receptor-specific ligands,
XX	useful for detecting tumors, inflammation etc., also therapeutic use of
PS	ligand inhibitors .
XX	
PS	Disclosure: Page 10; 26pp; German.
XX	
CC	This invention describes a novel diagnostic agent (A) comprising at least
CC	two different ligands (I) for receptors (II) that are implicated in
CC	disease. (A) are used for the diagnosis of tumors (especially colorectal
CC	or prostatic), organ rejection, inflammation and autoimmune diseases.
CC	Also inhibitors of (I) are used therapeutically against tumors (and their
CC	metastases), inflammation (particularly bronchial asthma or chronic bowel
CC	inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC	where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC	endocrine, motor or urogenital systems or skin are affected, and bone
CC	marrow diseases. The products of the invention are chemokine derivatives
CC	which have cytostatic, antiinflammatory, antiproliferative,
CC	immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC	Chemokines act on specific tumor and inflammatory cells through a
CC	constellation of chemokine receptors (CR), which control migration and
CC	proliferation of these cells. AMG8045-AMG8012 represent human chemokine
CC	fragments used to illustrate the method of the invention.
XX	
SQ	Sequence 352 AA:
Query Match	85.4%; Score 958; DB 22; Length 352;
Best Local Similarity	100.0%; Pred. No. 1e-105;
Matches 184; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MDYOVSPPYDINYNTSEPCOKINKOIAKRLPPLYSIVFTGFVGNMLVILINCKR 60
DB	1 MDYOVSPPYDINYNTSEPCOKINKOIAKRLPPLYSIVFTGFVGNMLVILINCKR 60
OY	61 LKSMTDIYLNLAINAISDLFFLLTPVPMAHYAAOMDPGMTCOLLTGLYFIGFGSIFETI 120
DB	61 LKSMTDIYLNLAINAISDLFFLLTPVPMAHYAAOMDPGMTCOLLTGLYFIGFGSIFETI 120
OY	121 LTTIDRYLAHVAVALKARTVTGCVTVSYITWWVAVFASLPGIIFTRSKOREGLHYCSS 180
DB	121 LTTIDRYLAHVAVALKARTVTGCVTVSYITWWVAVFASLPGIIFTRSKOREGLHYCSS 180
OY	181 HFPY 184
DB	181 HFPY 184
RESULT 10	
ID	AAB82948
AC	AAB82948 standard; Protein: 352 AA.
AC	AAB82948;
DT	21-DEC-2001 (first entry)
DE	Human HIV-1 co-receptor CCR5.

CC chemokine receptor that has been designated CCR5. The sequence was deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant (see W238340 of CCR5 was also identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains of HIV.

XX Sequence 352 AA;

Query Match 85.4%; Score 958; DB 19; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-105; Indels 0; Gaps 0;
Matches 184; Conservative 0; Mismatches 0;

QY 1 MDVQSSPIVDINITYSEPCCKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
DB 1 MDVQSSPIVDINITYSEPCCKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60
QY 61 LKSMIDYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMQLTGLYFGFSGIFETI 120
DB 61 LKSMIDYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMQLTGLYFGFSGIFETI 120
QY 121 LITDRIYAAVHAFAKARTVTEGVVSVITWVAFAASLPGLIFRSQEGHLYTCSS 180
DB 121 LITDRIYAAVHAFAKARTVTEGVVSVITWVAFAASLPGLIFRSQEGHLYTCSS 180
QY 181 HPPY 184
DB 181 HPPY 184

RESULT 7
AAW88232 standard; Protein; 352 AA.

XX AAW88232;

DT 15-MAR-1999 (first entry)

XX HIV-1 co-receptor CCR5.

XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;

KW gene therapy; human.

XX Homo sapiens.

XX Location/Qualifiers

FT 32..56 /note= "transmembrane domain 1"

FT 67..87 /note= "transmembrane domain 2"

FT /note= "transmembrane domain 2"

FT /note= "corresponds to Tgt (Cys) in wild-type CCR5, TGA (Stop) in CCR5m303"

FT 103..124 /note= "transmembrane domain 3"

FT 142..167 /note= "transmembrane domain 4"

FT 200..223 /note= "transmembrane domain 5"

FT 236..260 /note= "transmembrane domain 6"

FT 275..301 /note= "transmembrane domain 7"

PN W09854317-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-EP03437.

XX 30-MAY-1997; 97US-0048057.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Arenzana Silesdedos F, Beretta A, Braun J, Quillent C;

XX WPI: 1999-059835/05.

XX N-PSDB: AAW84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection

XX Disclosure; Page 34-35; 55pp; English.

This is the amino acid sequence of wild-type human CCR5, which serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the identification of a CCR5 variant (see AAW88231), designated CCR5m303, comprising the first two transmembrane domains of wild-type CCR5, but lacking transmembrane domains 3-7. The presence of the CCR5m303 variant with the wild type CCR5 allele shows a positive correlation with resistance to infection with M-tropic HIV-1. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAW84127-36) are provided for use in diagnostic methods for detecting HIV-1 infection of a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface.

XX Sequence 352 AA;

Query Match 85.4%; Score 958; DB 20; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-105; Indels 0; Gaps 0;
Matches 184; Conservative 0; Mismatches 0;

QY 1 MDVQSSPIVDINITYSEPCCKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60

DB 1 MDVQSSPIVDINITYSEPCCKINVKQIAARLLPPLSLVFIFGVGNMLVILLINCKR 60

QY 61 LKSMIDYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMQLTGLYFGFSGIFETI 120

DB 61 LKSMIDYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMQLTGLYFGFSGIFETI 120

QY 121 LITDRIYAAVHAFAKARTVTEGVVSVITWVAFAASLPGLIFRSQEGHLYTCSS 180

DB 121 LITDRIYAAVHAFAKARTVTEGVVSVITWVAFAASLPGLIFRSQEGHLYTCSS 180

QY 181 HPPY 184

DB 181 HPPY 184

RESULT 8
ABB56342 standard; Protein; 352 AA.

XX ABB56342;

AC 18-FEB-2002 (first entry)

XX Non-endogenous human GPCR protein, SEQ ID NO: 477.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;

XX constitutively activated GPCR; agonist; disease.

KW

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OM protein - protein search, using SW model

Run on: June 3, 2003, 15:16:36 ; Search time 19.7178 Seconds
(without alignment)
1048.235 Million cell updates/sec

Title: US-09-939-226-6

Perfect score: 1122
Sequence: 1 MDQVSSPIVDINYTSEPC.....AACGHLILGNPKNSASVSK 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	958	85.4	352 2 A43113	chemokine (C-C) re
2	694	61.9	360 2 JC2443	chemokine (C-C) re
3	694	61.9	374 2 I38450	chemokine (C-C) re
4	598	53.3	355 2 A45177	chemokine (C-C) re
5	573.5	51.1	355 2 I49339	macrophage inflamm
6	547.5	48.8	360 2 A57160	chemokine (C-C) re
7	546.5	48.7	360 2 JC4587	chemokine (C-C) re
8	535.5	47.7	359 2 I49341	MIP-1 alpha recept
9	506.5	45.1	355 2 G02436	chemokine (C-C) re
10	489.5	43.6	356 2 I49340	MIP-1 alpha recept
11	449	40.0	383 2 S55594	G protein-coupled
12	427.5	38.1	355 2 JC5067	G protein-coupled
13	386	34.4	354 2 I58186	probable G protein
14	378	33.7	344 2 JC5942	chemokine receptor
15	365	32.5	355 2 JC4304	orphan G protein-c
16	345.5	30.8	378 2 B55735	lymphocyte-specifi
17	343.5	30.5	378 2 A55735	G protein-coupled
18	333.5	29.7	378 2 A45680	G protein-coupled
19	331.5	29.5	352 2 A45747	neuropeptide Y/pep
20	326	29.1	353 2 S28787	neuropeptide Y/pep
21	325.5	29.0	352 2 G00048	angiotensin II rec
22	321.5	28.7	359 2 I51372	angiotensin II rec
23	320	28.5	359 2 JC5068	G protein-coupled
24	317	28.3	359 2 JC1194	angiotensin II rec
25	314	28.0	359 2 A42656	angiotensin II rec
26	312	27.8	359 2 JC1104	angiotensin II rec
27	312	27.8	359 2 I39418	angiotensin II rec
28	311	27.7	359 2 JC2134	angiotensin II rec
29	310	27.6	359 2 S15403	angiotensin II rec

30	309	27.5	359 2 JH0621	angiotensin II rec
31	308	27.5	359 2 A48857	angiotensin II rec
32	307	27.4	359 2 S44425	angiotensin II rec
33	306	27.3	359 2 J01516	angiotensin II rec
34	291	25.9	350 2 JN0621	G protein-coupled
35	287.5	25.6	367 2 JF0349	interferon-inducib
36	283	25.2	362 2 JN0694	angiotensin II rec
37	276	24.6	333 2 I65989	G protein-coupled
38	276	24.6	363 2 I57955	somatostatin recep
39	276	24.6	364 2 JN0763	somatostatin recep
40	274.5	24.5	359 2 A48921	interleukin-8 rece
41	273.5	24.4	384 2 A47249	brain-specific som
42	270.5	24.1	388 2 JN0605	somatostatin recep
43	269	24.0	360 2 A53611	interleukin-8 rece
44	267	23.8	363 2 I57940	somatostatin recep
45	265	23.6	355 2 J01231	interleukin-8 rece

ALIGNMENTS

RESULT 1
A43113
Chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence-revision 12-Jul-1996 #text-change 20-Jun-2000
C:Accession: A43113; S:1808; A:58834; A:58832; G02653; A:58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine rece
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Llesand, C.; Farber, C.M.; Sarag
M.; Imal, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele
A:Reference number: S71808; MUID:9645670; PMID:8751444
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184; IKDHLGACPAACGHLILGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X93393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A:Note: This frameshift mutation results in a non-functional receptor but confers a d
nd may have had a selective advantage by conferring resistance to Yersinia plague inf
R:Combadere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AA81071.1; PID:g1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-89; 'L', '91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemok
A:Reference number: A58833; MUID:96291862; PMID:8663314

A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:g1457945; PUD:1457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30575) and dual-tropic strains of HIV-1 bind to a complex of chemokine (C) receptors:
C:Genetics:
A:Gene: GDB:CMKR5; CCR5; CCR-5; CC-CR-5; CCR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A:Note: probably acts to control granulocyte proliferation and differentiation
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:144-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:20-269,101-178/Disulfide bonds: #status predicted
F:326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

```

Query Match      85.4%; Score 958; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-80;
Matches 184; Conservative 0; Mismatches 0; Gaps 0

```

Qy	1	MDYOVSSTIYDINITYTSPCKINKOJAARLLPPLYSIVFEGFVGNMLVILLINCKR	60
Db	1	MDYOVSSTIYDINITYTSPCKINKOJAARLLPPLYSIVFEGFVGNMLVILLINCKR	60
Qy	61	LKSMTDIYLMLAISDFELLTPPMWYAAAOQMGNTMCOLLGLYFIGFSGIFETI	120
Db	61	LKSMTDIYLMLAISDFELLTPPMWYAAAOQMGNTMCOLLGLYFIGFSGIFETI	120
Qy	121	LITDRIYAAVHAFAKARTVTCGVTSVITWVAVFAASLPGIITFNSQKGLHYTCSS	180
Db	121	LITDRIYAAVHAFAKARTVTCGVTSVITWVAVFAASLPGIITFNSQKGLHYTCSS	180
Qy	181	HPY 184	
Db	181	HPY 184	

```

RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000.
C:Accession: JC2443; I38663
R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A:Reference number: JC2443; MUID:94324942; PMID:8048929
A:Accession: JC2443
A:Molecule type: mRNA
A:Residues: 1-360 <YAM>
A:Cross-references: DDBJ:D29984; NID:9531246; PIDN:BA06253.1; PID:9531247
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant prot
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: 138463
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U03905; NID:9472557; PIDN:AA19120.1; PID:9472558
A:Genetics:

```

A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMTM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr
F:43-70/Domain: transmembrane #status predicted <TM1>
F:81-100/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:207-226/Domain: transmembrane #status predicted <TM5>
F:244-268/Domain: transmembrane #status predicted <TM6>
F:287-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:113-190/Disulfide bonds: #status predicted

Query Match	61.9%	Score 694	DB 2	Length 360
Best Local Similarity	75.9%	Pred. No. 2	4e-56	
Matches 132	Conservative 17	Mismatches 23	Indels 2	Gaps 1

0y 10 YDIINYTTSPECCOKINVKOIAARLLIPLYSLVFIEFGVGNMLVILLINCRLKSTSDIYL 69
Dbb 24 EDYDY--GAPCHKEFDVKQIGAGLPPILSYLVFIEFGVGNMLVLILLINCKRLKCLTDIYL 81

[illegible]

```

Qy      130 VHAVFALKARTVTEGVVTSVTWVAVFASPLPGIIFTRSQEGELHYTCSSHPF 183
      :|||||
Db      142 IHAVFALKARTVTEGVVTSVTWLVAVFASPLPGIIFTRKQKQEDSVVYCGPYFP 195

```

RESULT 3
138450

N:Alternative names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte C
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999

Richardo, I.F., Myers, S.J., Herman, A., Francis, C., Connolly, A.J., Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A:Accession: 138450
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-574 (MS)
A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
C:Genetics:
A:Gene: GDB:CMKBR2

A:Cross-references: GDB:337364; OMLM:60126/
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr

F.74-86/Domain	transmembrane	#status	predicted	<TM>
F.79-89/Domain	transmembrane	#status	predicted	<TM2>
F.115-136/Domain	transmembrane	#status	predicted	<TM4>
F.154-178/Domain	transmembrane	#status	predicted	<TM4>

F.1.208-266/Domain:	transmembrane
F.1.244-265/Domain:	transmembrane
F.292-309/Domain:	transmembrane
F.14/Binding site:	carbohydrate
(Asn) (covalent)	#status predicted

Query Match	61.9%	Score 694;	DB 2;	length 374;
Best local Similarity	75.9%	Pred. No. 2	5e-56;	
F:32-277,113-190/Disulfide bonds:		#status predicted		

Matches	132;	Conservative	17;	Mismatches	23;	Indels	2;	Gaps	1;
10	YDINNTSEPCOKINVKIARLLPLPLYSLETFEFGVGNLVTLLINCKRLKSMDDIYL	69							

Db 24 FDYDY - GACPCHKFDYKQIGAQLLPEPLYSLVEIFGFGVGNMLVLLILNCKKCLKCLTDIYL 81

Qy 70 LNLAIISDFELLTVBFWAHYAAQWDEGNMCQLTGLYETIGFSGIIFIIILLTIDRYLA 129

QY 2 DVOVSSPIIDINTYSE---PCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILIN 57
 Db 8 DTVLDSIYS-NVYLESPKPKCTKEGKAFGLFLPPLYSLVIFGGLGNSVYVLFK 66
 QY 58 CRKSKMTDYLINLAISDLFELLYPFAHVAQAQMDGNTMCGLLTGLYFGFSGIT 117
 Db 67 YKRLKMTDYLINLAISDLFELLYPFAHVAQAQMDGNTMCGLLTGLYFGFSGIT 126
 QY 118 FILLIDRYLAIVHVAFAKATVGVTSVITWVAFAVSLPGIIFTRSQEGHLYT 177
 Db 127 FVWLSIDRYLAIVHVAFAKATVGVTSVITWVAFAVSLPGIIFTRSQEGHLYT 186
 QY 178 CSCHF 182
 Db 187 CKTKY 191

RESULT 7
 JCA587
 Chemokine (C-C) receptor 4 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C:Accession: JCA587
 R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Blochem. Biophys. Res. Commun. 218, 337-343, 1996
 A>Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A:Reference number: JCA587; MUID:96136324; PMID:8573157
 A:Accession: JCA587
 A:Molecule type: mRNA
 A:Residues: 1-360 <RHO>
 A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CA62372.1; PID:g1167852
 A:Experimental source: thymus
 C:Genetics:
 A:Gene: cc cr-4
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F:123,194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:172,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 48.7%; Score 546.5; DB 2; Length 360;
 Best Local Similarity 55.9%; Pred. No. 8.8e-43;
 Matches 99; Conservative 36; Mismatches 39; Indels 3; Gaps 1;

QY 9 IYDINYY--TSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKRKSMT 65
 Db 15 VNSYTFYFESMPKPKCTKEGKAFGLFLPPLYSLVIFGGLGNSVYVLFKTKRKSMT 74
 QY 66 DYLINLAISDLFELLYPFAHVAQAQMDGNTMCGLLTGLYFGFSGIFILLITD 125
 Db 75 DYLINLAISDLFELLYPFAHVAQAQMDGNTMCGLLTGLYFGFSGIFILLITD 134
 QY 126 RFLAVHVAFAKATVGVTSVITWVAFAVSLPGIIFTRSQEGHLYTCSCHF 182
 Db 135 RFLAVHVAFAKATVGVTSVITWVAFAVSLPGIIFTRSQEGHLYTCSCHF 191

RESULT 8
 JCA587
 MIP-1 alpha receptor like-2 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 C:Accession: JCA587
 R:Guo, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A>Title: Cloning and differential tissue-specific expression of three mouse beta chemok
 A:Reference number: JCA587; MUID:95340546; PMID:7542241
 A:Accession: JCA587
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>

A:Cross-references: EMBL:U028406; NID:g881551; PID:g881552
 C:Superfamily: vertebrate rhodopsin

Query Match 47.7%; Score 535.5; DB 2; Length 359;
 Best Local Similarity 57.9%; Pred. No. 9e-42;
 Matches 99; Conservative 31; Mismatches 40; Indels 1; Gaps 1;

QY 14 YTSSEPCQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKRKSMTDYLINLA 73
 Db 22 YKAPCEKRIKELDSWLLPPLYSLVIFGGLGNSVYVLFKTKRKSMTDYLINLA 81
 QY 74 ISDLFELLYPFAHVAQAQMDGNTMCGLLTGLYFGFSGIFILLITDRLAVHVA 132
 Db 82 ISDLFELLYPFAHVAQAQMDGNTMCGLLTGLYFGFSGIFILLITDRLAVHVA 141
 QY 133 AVFALKATVGVTSVITWVAFAVSLPGIIFTRSQEGHLYTCSCHF 183
 Db 142 AVFALKATVGVTSVITWVAFAVSLPGIIFTRSQEGHLYTCSCHF 192

RESULT 9
 G02436
 Chemokine (C-C) receptor 3 - human
 N:Alternate names: C-C CKR-3
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
 C:Accession: G02436; A57237
 R:Ponath, P.D.
 Submitted to the EMBL Data Library, February 1996
 A:Reference number: H01272
 A:Accession: G02436
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <PON>
 A:Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561
 R:Combaladre, C.; Anuja, S.K.; Murphy, P.M.
 J. Biol. Chem. 270, 16491-16494, 1995
 A>Title: Cloning and functional expression of a human eosinophil CC chemokine recepto
 A:Reference number: A57237; MUID:95348056; PMID:7622448
 A:Accession: A57237
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
 A:Cross-references: GB:U28694; NID:g1199557; PIDN:AAC50469.1; PID:g1199580
 A>Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504
 C:Genetics:
 A:Gene: GDB:CMKBR3
 A:Cross-references: GDB:579624; OMIM:601268
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
 F:56-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:205-223/Domain: transmembrane #status predicted <TM5>
 F:240-261/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:24-273, 106-183/Disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi

Query Match 45.1%; Score 506.5; DB 2; Length 355;
 Best Local Similarity 57.6%; Pred. No. 4.2e-39;
 Matches 95; Conservative 32; Mismatches 37; Indels 1; Gaps 1;

QY 20 CQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKRKSMTDYLINLAISDLF 79
 Db 24 CQKINVKQIAARLLPPLYSLVIFGFGVGNMLVILINCKRKSMTDYLINLAISDLF 83
 QY 80 ILTVFPMHVAQAQMDGNTMCGLLTGLYFGFSGIFILLITDRLAVHVAFAK 138
 Db 84 LTVLPWHTVYRGHNMVGHGCKLLSGYHGLYSELFILLITDRLAVHVAFAK 143

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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:09:40 : Search time 9.85891 Seconds

(without alignments)
904.503 Million cell updates/sec

Title: US-09-939-226-6

Perfect score: 1122
Sequence: 1 MDYOVSSPTIDINVTSEPC.....ACCHGLLGNPKNSASVSK 215

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	958	85.4	352 1	CKR5_HUMAN
2	952	84.8	352 1	CKR5_PANTR
3	947	84.4	352 1	CKR5_PONPY
4	942	84.0	352 1	CKR5_GORGO
5	938	83.6	352 1	CKR5_PYGIBI
6	938	83.6	352 1	CKR5_PYGIBI
7	938	83.6	352 1	CKR5_TRAFR
8	938	83.6	352 1	CKR5_TRAFR
9	936	83.4	352 1	CKR5_HYLE
10	933	83.2	352 1	CKR5_PACMA
11	933	83.2	352 1	CKR5_PACMA
12	928	82.7	352 1	CKR5_CERTO
13	916	81.6	352 1	CKR5_CERTO
14	786	70.1	354 1	CKR5_MOUSE
15	775	69.1	354 1	CKR5_MOUSE
16	715.5	63.8	373 1	CKR2_MOUSE
17	714.5	63.7	373 1	CKR2_MOUSE
18	694	61.9	374 1	CKR2_MOUSE
19	688	61.3	360 1	CKR2_MOUSE
20	598	53.3	355 1	CKR1_MOUSE
21	570.5	50.8	355 1	CKR1_MOUSE
22	562	50.1	355 1	CKR1_MOUSE
23	547.5	48.8	360 1	CKR4_MOUSE
24	546.5	48.7	359 1	CKR4_MOUSE
25	535.5	47.7	359 1	CKR3_MOUSE
26	535.5	47.7	359 1	CKR3_MOUSE
27	516.5	46.0	358 1	CKR3_MOUSE
28	506.5	45.1	355 1	CKR3_MOUSE
29	499.5	44.5	355 1	CKR3_MOUSE
30	489.5	43.6	356 1	CKR3_MOUSE
31	489.5	43.6	356 1	CKR3_MOUSE
32	431	38.4	353 1	CKR8_MOUSE
33	427.5	38.1	353 1	CKR8_MOUSE

34	424	37.8	356 1	CKR8_MOUSE
35	386	34.4	354 1	C3X1_MOUSE
36	383	34.1	354 1	C3X1_MOUSE
37	370	33.0	369 1	CKR9_MOUSE
38	365	32.5	355 1	CKR1_MOUSE
39	363	32.4	357 1	CKR9_MOUSE
40	345.5	30.8	378 1	CKR7_MOUSE
41	342.5	30.5	378 1	CKR7_MOUSE
42	334.5	29.8	352 1	CCR4_MOUSE
43	331.5	29.5	352 1	CCR4_MOUSE
44	331.5	29.5	352 1	CCR4_MOUSE
45	330.5	29.5	384 1	CKD6_MOUSE

ALIGNMENTS

RESULT 1:
ID CKR5_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; O9UPA4;
DT 01-OCT-1996 (Ref. 34, Created)
DT 01-OCT-1996 (Ref. 34, Last sequence update)
DE 15-JUN-2002 (Ref. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C-CKR-5) (CCR-5) (CCR5)
DE (HIV-1 fusion co-receptor) (CHEM13) (CD195 antigen).
GN CCR5 OR CCR5R5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE-96241590; PubMed-8639485;
RA Samson M., Labbe O., Molleau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
RT C-C chemokine receptor gene";
RL Biochemistry 35:3362-3367(1996).
[2]
RP MEDLINE-96251862; PubMed-8663114;
RA Report C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
RT C-C chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha";
RL J. Biol. Chem. 271:17161-17166(1996).
[3]
RP MEDLINE-96295970; PubMed-8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RT RANTES";
RL J. Leukoc. Biol. 60:147-152(1996).
[4]
RP MEDLINE-96295970; PubMed-8699119;
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mendis E., Schutz R.,
RA Gao L., La Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagipanti J.L.;
RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
[5]
RP MEDLINE-98001387; PubMed-9343222;
RA Kumann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses";
RL J. Virol. 71:8642-8656(1997).

[6]
 RN SEQUENCE FROM N.A., AND POLYMORPHISMS.
 RP MEDLINE-98022612; PubMed-9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
 RL Aids Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98049523; PubMed-9388201;
 RT Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 with 5'-end heterogeneity, dual promoter usage, and evidence for
 RT polymorphisms within the regulatory regions and noncoding exons.";
 RL J. Biol. Chem. 272:30662-30671(1997).
 RN [8]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Issatras H., Theodorou I.,
 RA Debre P.;
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 RN [9]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA MEDLINE-96260017; PubMed-8649511;
 RA Deng H., Liu R., Elmeier W., Choe S., Unutmaz D., Burkhardt M.,
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Pelper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 RT HIV-1";
 RL Nature 381:661-666(1996).
 RN [10]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA MEDLINE-96260018; PubMed-8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koop R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RT CC-CKR 5.";
 RL Nature 381:667-673(1996).
 RN [11]
 RP SULFATION.
 RA MEDLINE-99189752; PubMed-10089882;
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 RT entry";
 RL Cell 96:667-676(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
 CC SYNCYTUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
 CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
 CC -1- PTM: SULFATION CONTRIBUTES TO THE EFFICIENCY OF HIV-1 ENTRY.
 CC -1- PTM: MODIFIED BY O-LINKED GLYCOSYLATION, BUT NOT BY N-LINKED
 CC GLYCOSYLATION.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF011500; AAB65700.1;
 DR EMBL; AF011501; AAB65701.1;
 DR EMBL; AF011502; AAB65702.1;
 DR EMBL; AF011503; AAB65703.1;
 DR EMBL; AF011505; AAB65705.1;
 DR EMBL; AF011506; AAB65706.1;
 DR EMBL; AF011507; AAB65707.1;
 DR EMBL; AF011508; AAB65708.1;
 DR EMBL; AF011509; AAB65709.1;
 DR EMBL; AF011510; AAB65710.1;
 DR EMBL; AF011511; AAB65711.1;
 DR EMBL; AF011512; AAB65712.1;
 DR EMBL; AF011513; AAB65713.1;
 DR EMBL; AF011514; AAB65714.1;
 DR EMBL; AF011515; AAB65715.1;
 DR EMBL; AF011516; AAB65716.1;
 DR EMBL; AF011517; AAB65717.1;
 DR EMBL; AF011518; AAB65718.1;
 DR EMBL; AF011519; AAB65719.1;
 DR EMBL; AF011520; AAB65720.1;
 DR EMBL; AF011521; AAB65721.1;
 DR EMBL; AF011522; AAB65722.1;
 DR EMBL; AF011523; AAB65723.1;
 DR EMBL; AF011524; AAB65724.1;
 DR EMBL; AF011525; AAB65725.1;
 DR EMBL; AF011526; AAB65726.1;
 DR EMBL; AF011527; AAB65727.1;
 DR EMBL; AF011528; AAB65728.1;
 DR EMBL; AF011529; AAB65729.1;
 DR EMBL; AF011530; AAB65730.1;
 DR EMBL; AF011531; AAB65731.1;
 DR EMBL; AF011532; AAB65732.1;
 DR EMBL; AF011533; AAB65733.1;
 DR EMBL; AF011534; AAB65734.1;
 DR EMBL; AF011535; AAB65735.1;
 DR EMBL; AF011536; AAB65736.1;
 DR EMBL; AF011537; AAB65737.1;
 DR EMBL; AF031237; AAB94735.1;
 DR EMBL; AF052539; AAD18131.1;
 DR Gene; HGNC:1606; CCR5.
 DR MIM: 601373;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1_1;
 DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW Polymorphism.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT MOD_RES 15 15
 FT VARIANT 10 10
 FT VARIANT 29 29
 FT VARIANT 31 31
 FT VARIANT 31 31

EXTRACELLULAR (POTENTIAL).
 1 (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 2 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 3 (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 4 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 5 (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 6 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 7 (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 BY SIMILARITY.
 SULFATION.
 SULFATION.
 SULFATION.
 Y -> D (IN INCR5-71A).
 A -> S (IN DBSNP:1800939).
 /FTID-VAR 003481.
 /FTID-VAR 011839.
 R -> H (IN INCR5-72A).

Query Match 85.4%; Score 958; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2,3e-53;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDVQSSPIIDYINSEPCOKINVOIAARLLPPLYSLVIFGFGNMLVILLINCKR 60
 DB 1 MDVQSSPIIDYINSEPCOKINVOIAARLLPPLYSLVIFGFGNMLVILLINCKR 60
 OY 61 LKSMTDIYLLNLALISDLFFLLVFPFAHVAQAQMDGNTWCQLLTGLYIFGFSGIFETI 120
 DB 61 LKSMTDIYLLNLALISDLFFLLVFPFAHVAQAQMDGNTWCQLLTGLYIFGFSGIFETI 120
 OY 121 LITIDRYLAVHVAHVAFLKATVTFGVVTSYITVAVFASLPGLITFRSQEGLHYTCSS 180
 DB 121 LITIDRYLAVHVAHVAFLKATVTFGVVTSYITVAVFASLPGLITFRSQEGLHYTCSS 180
 OY 181 HEPY 184
 DB 181 HEPY 184

RESULT 2
 CCR5_PANTR STANDARD; PRT; 352 AA.
 AC P56440; 002778;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97268687; Pubmed-9108095;
 RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Cord M.,
 RA Pelton S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT strain immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98022612; Pubmed-9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97426118; Pubmed-9282822;
 RA Zacharova V., Zachar V., Goussin A.S.;
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 RT HIV type 1 host";
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98090115; Pubmed-9430250;
 RA Pretet J.-L., Zarb A., Girard M., Guillet J.-G., Buter C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 CC - FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).

CC EMBL: AF005663; AAB62557.1; -
 DR EMBL: U94328; AAB58446.1; -
 DR EMBL: AF011542; AAB65742.1; -
 DR EMBL: U97666; AAC51670.1; -
 DR EMBL: AF011540; AAB65740.1; -
 DR EMBL: U9797; AAC03717.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 88
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT TRANSMEM 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 123 123
 SQ SEQUENCE 352 AA; 40539 MW; 4A33698B80FE34C CRC64;

Query Match 84.8%; Score 952; DB 1; Length 352;
 Best Local Similarity 98.9%; Pred. No. 5,4e-53;
 Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDVQSSPIIDYINSEPCOKINVOIAARLLPPLYSLVIFGFGNMLVILLINCKR 60
 DB 1 MDVQSSPIIDYINSEPCOKINVOIAARLLPPLYSLVIFGFGNMLVILLINCKR 60
 OY 61 LKSMTDIYLLNLALISDLFFLLVFPFAHVAQAQMDGNTWCQLLTGLYIFGFSGIFETI 120
 DB 61 LKSMTDIYLLNLALISDLFFLLVFPFAHVAQAQMDGNTWCQLLTGLYIFGFSGIFETI 120
 OY 121 LITIDRYLAVHVAHVAFLKATVTFGVVTSYITVAVFASLPGLITFRSQEGLHYTCSS 180
 DB 121 LITIDRYLAVHVAHVAFLKATVTFGVVTSYITVAVFASLPGLITFRSQEGLHYTCSS 180
 OY 181 HEPY 184
 DB 181 HEPY 184

RESULT 3
 CCR5_PONPY STANDARD; PRT; 352 AA.
 AC 097881;
 DT 30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C Chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CKR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
[1]
SEQUENCE FROM N.A.
MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates."
Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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or send an email to license@isb-slb.ch).

CC EMBL: AF075446; AAD19858.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 1 31
FT DOMAIN 59 58
FT TRANSMEM 69 68
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULF 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40527 MW; F4E2FA7135AF658A CRC64;

Query Match 84.4%; Score 947; DB 1; Length 352;
Best Local Similarity 98.4%; Pred. No. 1,1e-52;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

121 LITDRIYLAIVHAVALKARTVTEGVNVSITWVAFAASLPGLITFSQKGLHYTCSS 180
181 HEPY 184
181 HEPY 184
181 HEPY 184

DB 121 LITDRIYLAIVHAVALKARTVTEGVNVSITWVAFAASLPGLITFSQKGLHYTCSS 180
QY 181 HEPY 184
DB 181 HEPY 184

RESULT 4
CCR5_GORGO STANDARD; PRT: 352 AA.
ID CCR5_GORGO
AC P56439; GORGO
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
[1]
SEQUENCE FROM N.A.
MEDLINE=97266687; PubMed=9108095;
Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
Pelger S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains."
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AF005659; AAB2553.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 58
FT TRANSMEM 69 68
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULF 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
SQ SEQUENCE 352 AA; 40515 MW; D0B6FCB9FE5EAC84 CRC64;

Query Match 84.0%; Score 942; DB 1; Length 352;
 Best Local Similarity 97.8%; Pred. No. 2.3e-55;
 Matches 180; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDYOVSSPTIDINTYTSPPCKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILLINCKR 60
 DB 1 MDYOVSSPTIDINTYTSPPCKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILLINCKR 60
 OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPNTMCOQLTGLYIFGFSGIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPNTMCOQLTGLYIFGFSGIFPII 120
 OY 121 LRTDRYLAVHAFALKARTVTEGVVTSVITVWVAFAASLPGIIFTRSQREGIHYTCSS 180
 DB 121 LRTDRYLAVHAFALKARTVTEGVVTSVITVWVAFAASLPGIIFTRSQREGIHYTCSS 180
 OY 181 HFPY 184
 DB 181 HFPY 184

RESULT 5
 CKR5_PYGBI STANDARD; PRT; 352 AA.
 ID CKR5_PYGBI
 AC 097880;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Pygathrix blueti (Black snub-nosed monkey) (Rhinothecus blueti).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 NC NCBI_Taxid=61621;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: AF075445; AAD19857.1;
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm1.1;
 DR PROSITE: PS00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 38 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 39 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT TRANSMEM 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT TRANSMEM 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 DR

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40585 MW; 4366f142730f938f CRC64;

Query Match 83.6%; Score 938; DB 1; Length 352;
 Best Local Similarity 96.2%; Pred. No. 4e-52;
 Matches 177; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYOVSSPTIDINTYTSPPCKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILLINCKR 60
 DB 1 MDYOVSSPTIDINTYTSPPCKINVKQIAARLLPPLYSLVFIFGFGVGNMLVILLINCKR 60
 OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPNTMCOQLTGLYIFGFSGIFPII 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDPNTMCOQLTGLYIFGFSGIFPII 120
 OY 121 LRTDRYLAVHAFALKARTVTEGVVTSVITVWVAFAASLPGIIFTRSQREGIHYTCSS 180
 DB 121 LRTDRYLAVHAFALKARTVTEGVVTSVITVWVAFAASLPGIIFTRSQREGIHYTCSS 180
 OY 181 HFPY 184
 DB 181 HFPY 184

RESULT 6
 CKR5_PYGBI STANDARD; PRT; 352 AA.
 ID CKR5_PYGBI
 AC 097882;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Pygathrix nemaeus (Dove langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 NC NCBI_Taxid=54133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: AF075448; AAD19860.1;
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 DR

DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
 DR PROSITE: PS00262; G_PROTEIN_REC_P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT TRANSMEM 59 68
 FT TRANSMEM 69 89
 FT TRANSMEM 90 102
 FT TRANSMEM 103 124
 FT TRANSMEM 125 141
 FT TRANSMEM 142 166
 FT TRANSMEM 167 198
 FT TRANSMEM 199 235
 FT TRANSMEM 236 260
 FT TRANSMEM 261 277
 FT TRANSMEM 278 301
 FT TRANSMEM 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 SQ SEQUENCE 352 AA; 40532 MW; FEA9D98D3B3861 CRC64;

Query Match
 Best Local Similarity 96.2%; Score 938; DB 1; Length 352;
 Matches 177; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDQVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSVLFEGVGNLVILLINCKR 60
 DB 1 MDQVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSVLFEGVGNLVILLINCKR 60
 QY 61 LKSMTDIYLNLAIISDLEFLLTPFWAHYAAQMPGNTMQLTGLYIFGFSIGFTI 120
 DB 61 LKSMTDIYLNLAIISDLEFLLTPFWAHYAAQMPGNTMQLTGLYIFGFSIGFTI 120
 QY 121 LITDIRYLAIVAHVAFALKARVTFGVTVSVITWVAVAFASLPGIIFTSQKGLHYTSS 180
 DB 121 LITDIRYLAIVAHVAFALKARVTFGVTVSVITWVAVAFASLPGIIFTSQKGLHYTSS 180
 QY 181 HPPY 184
 DB 181 HPPY 184

RESULT 7
 CCR5_TRAFR STANDARD; PRT; 352 AA.

AC 097878;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CR-5) (CC-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus.
 NCBI_TaxID=54180;
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: AF075442; AAD19854.1; -;
 DR InterPro: IPR00276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
 DR PROSITE: PS00262; G_PROTEIN_REC_P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT TRANSMEM 59 68
 FT TRANSMEM 69 89
 FT TRANSMEM 90 102
 FT TRANSMEM 103 124
 FT TRANSMEM 125 141
 FT TRANSMEM 142 166
 FT TRANSMEM 167 198
 FT TRANSMEM 199 235
 FT TRANSMEM 236 260
 FT TRANSMEM 261 277
 FT TRANSMEM 278 301
 FT TRANSMEM 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match
 Best Local Similarity 96.2%; Score 938; DB 1; Length 352;
 Matches 177; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDQVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSVLFEGVGNLVILLINCKR 60
 DB 1 MDQVSSPIYDINTYSEPCOKINVKQIAARLLPPLYSVLFEGVGNLVILLINCKR 60
 QY 61 LKSMTDIYLNLAIISDLEFLLTPFWAHYAAQMPGNTMQLTGLYIFGFSIGFTI 120
 DB 61 LKSMTDIYLNLAIISDLEFLLTPFWAHYAAQMPGNTMQLTGLYIFGFSIGFTI 120
 QY 121 LITDIRYLAIVAHVAFALKARVTFGVTVSVITWVAVAFASLPGIIFTSQKGLHYTSS 180
 DB 121 LITDIRYLAIVAHVAFALKARVTFGVTVSVITWVAVAFASLPGIIFTSQKGLHYTSS 180
 QY 181 HPPY 184
 DB 181 HPPY 184

RESULT 8
 CCR5_TRAFR STANDARD; PRT; 352 AA.

AC 097879;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CR-5) (CC-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Trachypithecus phayrei (Phayre's leaf monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;


```

DB 61 LKSMIDYILNLAISDLFLVTPFAHVAAMQMPGNTMQLGLGYIFGFSGIFFTI 120
QY 121 LITIDRYLAIVAHVAFKARVTGVTGVTIVVAVAFSLPGIIFTRSQKGLHYTCSS 180
DB 121 LITIDRYLAIVAHVAFKARVTGVTGVTIVVAVAFSLPGIIFTRSQKGLHYTCSS 180
QY 181 HEPY 184
DB 181 HEPY 184

RESULT 10
CRK5_MACMU STANDARD: PRT: 352 AA.
ID CRK5_MACMU STANDARD: PRT: 352 AA.
AC P79A36; 002746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5).
OS CCR5 OR CCR5R5.
OS Macaca mulatta (Rhesus macaque).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=90323394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239."
RT J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060663;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry."
RT J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=21554176; PubMed=11461684;
RA Marquies B.J., Haer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RT AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amodeo A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
DB 61 LKSMIDYILNLAISDLFLVTPFAHVAAMQMPGNTMQLGLGYIFGFSGIFFTI 120
QY 121 LITIDRYLAIVAHVAFKARVTGVTGVTIVVAVAFSLPGIIFTRSQKGLHYTCSS 180
DB 121 LITIDRYLAIVAHVAFKARVTGVTGVTIVVAVAFSLPGIIFTRSQKGLHYTCSS 180
QY 181 HEPY 184
DB 181 HEPY 184

RESULT 11
CRK5_PAPHA STANDARD: PRT: 352 AA.
ID CRK5_PAPHA STANDARD: PRT: 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5).

```


DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 KW DOMAIN 1
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT VARIANT 2 2
 FT VARIANT 3 3
 FT VARIANT 25 25
 FT VARIANT 100 100
 FT VARIANT 107 107
 FT VARIANT 134 134
 FT VARIANT 146 146
 FT VARIANT 340 340
 FT SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;
 Query Match 82.7%; Score 928; DB 1; Length 352;
 Best Local Similarity 95.7%; Pred. No. 1.7e-51;
 Matches 176; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MDYVSSPYDINIVSEPCOKINVOIARLLPPLYSIVETFGFVGNMVLILINCKR 60
 DB 1 MDYVSSPYDIDYVSEPCOKINVOIARLLPPLYSIVETFGFVGNMVLILINCKR 60
 QY 61 LKSMIDYLLNLALISDLFFLLVFPWAHYAAQWDFGNTMCOQLTGLYIFGFSGIFFII 120
 DB 61 LKSMIDYLLNLALISDLFFLLVFPWAHYAAQWDFGNTMCOQLTGLYIFGFSGIFFII 120
 QY 121 LITIDRYLAVHVAHFALRKARTVEGVTSVITMVVAVFASLPGLIFTRSORGLHYTCSP 180
 DB 121 LITIDRYLAVHVAHFALRKARTVEGVTSVITMVVAVFASLPGLIFTRSORGLHYTCSP 180
 QY 181 HEPY 184
 DB 181 HEPY 184
 RESULT 13
 CRRS_CERAE STANDARD: PRT; 352 AA.
 AC P56493;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS5).
 GN CCR5 OR CCR5.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 NCBI_Taxid=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;

RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses";
 RL J. Virol. 71:8642-8656(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
 RT "CDNA sequence of African green monkey CCR-5 chemokine receptor
 RT gene";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL: U83324; AAC51795.1; -
 CC EMBL: U83325; AAC51796.1; -
 CC EMBL: AB015944; BAA31328.1; -
 CC InterPro: IPR00276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW Polymorphism.
 KW DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 15 15
 FT VARIANT 14 14
 FT VARIANT 352 352
 FT SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;
 Query Match 81.6%; Score 916; DB 1; Length 352;
 Best Local Similarity 95.1%; Pred. No. 9.4e-51;
 Matches 175; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDYVSSPYDINIVSEPCOKINVOIARLLPPLYSIVETFGFVGNMVLILINCKR 60
 DB 1 MDYVSSPYDIDYVSEPCOKINVOIARLLPPLYSIVETFGFVGNMVLILINCKR 60
 QY 61 LKSMIDYLLNLALISDLFFLLVFPWAHYAAQWDFGNTMCOQLTGLYIFGFSGIFFII 120
 DB 61 LKSMIDYLLNLALISDLFFLLVFPWAHYAAQWDFGNTMCOQLTGLYIFGFSGIFFII 120

OY 121 LITDRILAVHAFALKARTVTCVITVAVANFASLPGIIFTRSGEGLHYTCCS 180
 DB 121 LITDRILAVHAFALKARTVTCVITVAVANFASLPGIIFTRSGEGLHYTCCS 180
 OY 181 HEPY 184
 DB 181 HEPY 184
 RESULT 14
 CKR5_MOUSE
 ID CKR5_MOUSE STANDARD: PRT: 354 AA.
 AC P51682; Q61867; P97405; O35313; P97308; O35891;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
 alpha receptor).
 GN CCR5 OR CCR5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SVJ; TISSUE-Spleen;
 RX MEDLINE-96205938; PubMed-8631787;
 RA Boring L., Gosling J., Montecarlo F.S., Luebs A.J., Tsou C.-L.,
 Chao I.P., Molecular cloning and functional expression of murine JE (monocyte
 chemottractant protein 1) and murine macrophage inflammatory protein
 RT 1alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.";
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6 X CBA; TISSUE-Thymus;
 RX MEDLINE-96276910; PubMed-8662890;
 RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "Cloning and characterization of a novel murine macrophage
 RT inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 271:14445-14451(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/Ola;
 RA Kuziel M.A., Beck M.A., Dawson T.C., Maeda N.;
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6, and NIH SV128; TISSUE-Liver, Kidney, and Spleen;
 RX MEDLINE-98001387; PubMed-934322;
 RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129;
 RX MEDLINE-97404635; PubMed-9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
 Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: U47036; AAC52454.1; -
 CC EMBL: X94151; CA63867.1; -
 CC EMBL: U68565; AAB37273.1; -
 CC EMBL: U83327; AAC53386.1; -
 CC EMBL: AF022990; AAC53389.1; -
 CC EMBL: AF019772; AAB1183.1; -
 CC EMBL: D83648; BAA12024.1; -
 CC MGD: MGI:107182; Cnhr5.
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCR_Rhodopsin.
 CC PROSITE: PS00237; G-PROTEIN_REC_P1.1; 1.
 CC PROSITE: PS00262; G-PROTEIN_REC_P1.2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 CC FT DOMAIN 1 32
 CC FT TRANSMEM 33 60
 CC FT DOMAIN 71 70
 CC FT TRANSMEM 71 91
 CC FT DOMAIN 92 104
 CC FT TRANSMEM 105 126
 CC FT DOMAIN 127 143
 CC FT TRANSMEM 144 168
 CC FT DOMAIN 169 200
 CC FT TRANSMEM 201 220
 CC FT DOMAIN 221 237
 CC FT TRANSMEM 238 262
 CC FT DOMAIN 263 279
 CC FT TRANSMEM 280 303
 CC FT DOMAIN 304 354
 CC FT DISULFID 103 180
 CC FT CARBOHYD 270 270
 CC FT VARIAT 11 11
 CC FT VARIAT 62 62
 CC FT VARIAT 65 66
 CC FT VARIAT 97 97
 CC FT VARIAT 109 109
 CC FT VARIAT 156 156
 CC FT VARIAT 160 160
 CC FT VARIAT 185 185
 CC FT VARIAT 213 213
 CC FT VARIAT 318 318
 CC FT VARIAT 337 337
 CC FT CONFLICT 3 3
 CC FT CONFLICT 80 80
 CC FT CONFLICT 145 145
 CC FT CONFLICT 190 190
 CC FT CONFLICT 208 208
 CC SO SEQUENCE 354 AA; 40863 MW; BAA6B942E8BF9CF0 CRC64;
 Query Match 70.1%; Score 786; DB 1; Length 354;
 Best Local Similarity 80.1%; Pred. No. 1,1e-42;
 Matches 149; Conservative 17; Mismatches 18; Indels 2; Gaps 1;
 OY 1 MDYVSSP--IYDNYTSEPCQKINVOIARLLPLYSLVFIFGVGNMLVYLILNC 58
 DB 1 MDYGVSTPTIYDIDIGKASAPCKINVOIAQLPLPSLVFIFGVGNMVFLLILSC 60
 OY 59 KRISMDYIYLLNLAISDLFLITVPPFAHYAAAMQMDGNCMTGLTGLTYIGPFGSGTF 118
 DB 61 KKLKSVYDIYLLNLAISDLFLITLTPFAHYAANEMIGNIMCKVETGVHYIGFGGTF 120

QY 119 ILLTIDRYLAVVAFAKARVTGVTSTVWVAFAFSLPGIIFTRSORKGLHYTC 178
 DB 121 ILLTIDRYLAVVAFAKARVTGVTSTVWVAFAFSLPGIIFTRSORKGLHYTC 180
 QY 179 SSHPPYK 184
 DB 181 SPHFLHQ 186
 RESULT 15
 CKR5_RAT STANDARD; PRT; 354 AA.
 AC 008556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
 alpha receptor).
 GN CCR5 OR CCR5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Histar; TISSUE=Brain;
 RC MEDLINE=98334064; PubMed=9670989;
 RA Speleas O., Gourmal N., Bodeke H.W.G.M., Sauter A., Fleblich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and
 RT upregulation of its mRNA in ischemic and endotoxemic rat brain.";
 RL J. Neurosci. Res. 53:16-28(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RC MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA Delibere C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: Y12009; CAA2737.1; -;
 CC EMBL: U77350; AAC03243.1; -;
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32
 FT TRANSSEM 33 60
 FT DOMAIN 61 70
 FT TRANSSEM 71 91
 FT DOMAIN 92 104
 FT TRANSSEM 105 126
 FT DOMAIN 127 143
 FT TRANSSEM 144 168
 FT DOMAIN 169 200
 FT TRANSSEM 201 220
 FT TRANSSEM 201 220

FT DOMAIN 221 227 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 238 262 6 (POTENTIAL).
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 280 303 7 (POTENTIAL).
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 103 180 BY SIMILARITY.
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C686D CRC64;
 Query Match 69.18; Score 775; DB 1; Length 354;
 Best Local Similarity 78.2%; Pred. No. 5.5e-42; Indels 2; Gaps 1;
 Matches 147; Conservative 18; Mismatches 21;
 QY 1 MDYOVSP--IYDINVTSEPCOKINVKQIAARLPLPLSLVFIEFGVGNMLVILLNC 58
 DB 1 MDRGSGIPTYITIDIDISMAKPCOKVNVKQIAQLPLPLSLVFIEFGVGNMAYVILLISC 60
 QY 59 KRLKSMTDIYLLNLAIISDLFFLLTPFWMAHYAAQNDFGNTKQQLTGXYFGFSGGIF 118
 DB 61 KRLKSMTDIYLLNLAIISDLFFLLTPFWMAHYAAQNDFGNTKQQLTGXYFGFSGGIF 120
 QY 119 ILLTIDRYLAVVAFAKARVTGVTSTVWVAFAFSLPGIIFTRSORKGLHYTC 178
 DB 121 ILLTIDRYLAVVAFAKARVTGVTSTVWVAFAFSLPGIIFTRSORKGLHYTC 180
 QY 179 SSHPPYK 186
 DB 181 SPHFLHQ 186
 Search completed: June 3, 2003, 15:19:39
 Job time : 10.8589 secs

OY 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
 DB 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
 OY 181 HEPYIKDSHLGAGPAACHGILLGNPKNSASVSK 215
 DB 181 HEPYIKDSHLGAGPAACHGILLGNPKNSASVSK 215

RESULT 2

O95NC5 PRELIMINARY; PRT; 352 AA.
 AC O95NC5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE C-C chemokine receptor 5.
 GN CCR5.
 OS Hylobates syndactylus (Slamang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9550;

RP [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 phylogeny";
 RT Submitted (Aug-1999) to the EMBL/Genbank/DBD databases.
 RL EMBL; AF177884; AAK43367.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 84.4%; Score 947; DB 6; Length 352;
 Best Local Similarity 98.4%; Pred. No. 1.9e-80;
 Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYVSSPIYDINTYTSEPCOKINVKQIAARLLPPLYSLVTFGFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINTYTSEPCOKINVKQIAARLLPPLYSLVTFGFGVGNMLVILLINCKR 60
 OY 61 LKSMIDYILNLAISDLFFLLVPPWAAHAAQMPGNTMCLLGLYIFGFGSIFFTI 120
 DB 61 LKSMIDYILNLAISDLFFLLVPPWAAHAAQMPGNTMCLLGLYIFGFGSIFFTI 120
 OY 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
 DB 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
 OY 181 HEPY 184
 DB 181 HEPY 184

RESULT 3

O18772 PRELIMINARY; PRT; 352 AA.
 AC O18772;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CCR5 receptor (Fragment).
 GN CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CHCCR5-142A;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
 DR EMBL; AF011541; AAB65741.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;

Query Match 84.2%; Score 945; DB 6; Length 352;
 Best Local Similarity 98.4%; Pred. No. 2.9e-80;
 Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYVSSPIYDINTYTSEPCOKINVKQIAARLLPPLYSLVTFGFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINTYTSEPCOKINVKQIAARLLPPLYSLVTFGFGVGNMLVILLINCKR 60
 OY 61 LKSMIDYILNLAISDLFFLLVPPWAAHAAQMPGNTMCLLGLYIFGFGSIFFTI 120
 DB 61 LKSMIDYILNLAISDLFFLLVPPWAAHAAQMPGNTMCLLGLYIFGFGSIFFTI 120
 OY 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
 DB 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAVAFASLPGIIFTRSQKGLHYTCSS 180
 OY 181 HEPY 184
 DB 181 HEPY 184

RESULT 4

O18771 PRELIMINARY; PRT; 352 AA.
 AC O18771;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CCR5 receptor (Fragment).
 GN CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CHCCR5-141A;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
 DR EMBL; AF011539; AAB65739.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 352 AA; 40466 MW; 3FFPAC7ABAED14FB CRC64;

Query Match 83.8%; Score 940; DB 6; Length 352;
 Best Local Similarity 97.8%; Pred. No. 8.6e-80;
 Matches 180; Conservative .3; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYVSSPIYDINTYTSEPCOKINVKQIAARLLPPLYSLVTFGFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINTYTSEPCOKINVKQIAARLLPPLYSLVTFGFGVGNMLVILLINCKR 60

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OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 120
    |||||||
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 120
OY 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 180
    |||||||
DB 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 180
OY 181 HFPY 184
    ||||
DB 181 HFPY 184

RESULT 5
095NC0 PRELIMINARY: PRT: 352 AA.
AC 095NC0:
DB 01-DEC-2001 (TREMBLREL. 19, Created)
DB 01-DEC-2001 (TREMBLREL. 19, Last sequence update)
DB 01-MAR-2002 (TREMBLREL. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates moloch (silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF177899; AAK43382.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR KM Receptor.
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 83.8%; Score 940; DB 6; Length 352;
Best Local Similarity 97.8%; Pred. No. 8.6e-80;
Matches 180; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDVSSPTDYIDYITSEPCOKINVKOIAARLLPPLYSLVFIFGVGNMVLILINCKR 60
    |||||||
DB 1 MDVSSPTDYIDYITSEPCOKINVKOIAARLLPPLYSLVFIFGVGNMVLILINCKR 60
OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 120
    |||||||
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 120
OY 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 180
    |||||||
DB 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 180
OY 181 HFPY 184
    ||||
DB 181 HFPY 184

RESULT 6
09XS99 PRELIMINARY: PRT: 352 AA.
AC 09XS99:
DB 01-NOV-1999 (TREMBLREL. 12, Created)
DB 01-NOV-1999 (TREMBLREL. 12, Last sequence update)
DB 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GORILLACR;
RX MEDLINE=99210133; PubMed=10195758;
RA Sakuma N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lai R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
DR EMBL: AF105291; AAD20560.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; GPCR_Rhodopsin.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR KM Receptor.
SQ SEQUENCE 352 AA; 40529 MW; 1BE6C68FE2E7AD0 CRC64;

Query Match 83.7%; Score 939; DB 6; Length 352;
Best Local Similarity 97.3%; Pred. No. 1.1e-79;
Matches 179; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDVSSPTDYIDYITSEPCOKINVKOIAARLLPPLYSLVFIFGVGNMVLILINCKR 60
    |||||||
DB 1 MDVSSPTDYIDYITSEPCOKINVKOIAARLLPPLYSLVFIFGVGNMVLILINCKR 60
OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 120
    |||||||
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 120
OY 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 180
    |||||||
DB 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMCOQLLTGLYFTGFSGIFPII 180
OY 181 HFPY 184
    ||||
DB 181 HFPY 184

RESULT 7
09TV50 PRELIMINARY: PRT: 352 AA.
AC 09TV50:
DB 01-MAY-2000 (TREMBLREL. 13, Created)
DB 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DB 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CC chemokine receptor type 5.
GN CCR5.
OS Pan troglodytes (chimpanzee).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1410;
RX MEDLINE=99335215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with HIV
RT carrier status in African nonhuman primates."
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1410;
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA Georges-Courbot M.C., Barre-Sinoussi F., Fomsgaard A.;
RL EMBL: AF035214; AAD44007.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

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DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 352 AA; 40461 MW; 2578A0E2C07A4A65 CRC64;

Query Match 83.6%; Score 938; DB 6; Length 352;
 Best Local Similarity 96.7%; Pred. No. 1.3e-79;
 Matches 178; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPYDINDYNTSEPCQKINVKQIARLLPLYSVIFFGVGNMVLILINCKR 60
 DB 1 MDYVSSPYDIDYNTSEPCQKINVKQIARLLPLYSVIFFGVGNLVLILINCKR 60
 QY 61 LKSMIDYLLNLAIISDLFFELLTPFWAHYAQAQMPDGNMTCOLLGLYFIFGSGIFETI 120
 DB 61 LKSMIDYLLNLAIISDLFFELLTPFWAHYAQAQMPDGNMTCOLLGLYFIFGSGIFETI 120
 QY 121 LITIDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 DB 121 LITIDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 QY 181 HFPY 184
 DB 181 HFPY 184

RESULT 8

Q95NC8 PRELIMINARY; PRT; 352 AA.

AC 095NC8; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5.
 GN CCR5.
 OS Colobus polykomos.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Colobus.
 OX NCBI_TaxID=9572;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 phylogeny."
 RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF177881; AAK43364.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 352 AA; 40578 MW; 4366F149C3B4938F CRC64;

Query Match 83.6%; Score 938; DB 6; Length 352;
 Best Local Similarity 96.2%; Pred. No. 1.3e-79;
 Matches 177; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPYDINDYNTSEPCQKINVKQIARLLPLYSVIFFGVGNMVLILINCKR 60
 DB 1 MDYVSSPYDIDYNTSEPCQKINVKQIARLLPLYSVIFFGVGNLVLILINCKR 60
 QY 61 LKSMIDYLLNLAIISDLFFELLTPFWAHYAQAQMPDGNMTCOLLGLYFIFGSGIFETI 120
 DB 61 LKSMIDYLLNLAIISDLFFELLTPFWAHYAQAQMPDGNMTCOLLGLYFIFGSGIFETI 120
 QY 121 LITIDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 DB 121 LITIDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 QY 181 HFPY 184
 DB 181 HFPY 184

RESULT 9

Q95NC6 PRELIMINARY; PRT; 352 AA.

AC 095NC6; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5.
 GN CCR5.
 OS Trachypithecus johni (hooded leaf monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus.
 OX NCBI_TaxID=66063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 phylogeny."
 RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF177883; AAK43366.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 352 AA; 40462 MW; 52824E032259F7F CRC64;

Query Match 83.6%; Score 938; DB 6; Length 352;
 Best Local Similarity 96.2%; Pred. No. 1.3e-79;
 Matches 177; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDYVSSPYDINDYNTSEPCQKINVKQIARLLPLYSVIFFGVGNMVLILINCKR 60
 DB 1 MDYVSSPYDIDYNTSEPCQKINVKQIARLLPLYSVIFFGVGNLVLILINCKR 60
 QY 61 LKSMIDYLLNLAIISDLFFELLTPFWAHYAQAQMPDGNMTCOLLGLYFIFGSGIFETI 120
 DB 61 LKSMIDYLLNLAIISDLFFELLTPFWAHYAQAQMPDGNMTCOLLGLYFIFGSGIFETI 120
 QY 121 LITIDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 DB 121 LITIDRYLAIVHAVFALKARTVFGVTSVITWVAVFASLPGIIFTRSQKGLHYTCSS 180
 QY 181 HFPY 184
 DB 181 HFPY 184

RESULT 10

Q9MZA3 PRELIMINARY; PRT; 352 AA.

AC 09MZA3; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE C-C chemokine receptor 5.
 GN CCR5.
 OS Hylobates agilis unko.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9583;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20317091; PubMed-10747879;
 RA Mummidi S., Bamsbad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
 RA Begum K., Galvis M.C., Kosteci V., Valente A.J., Murthy K.K.,
 RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.,
 RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
 and mRNA. Potential roles for haplotype and mRNA diversity,
 RT differential haplotype-specific transcriptional activity, and altered
 RT transcription factor binding to polymorphic nucleotides in the

RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL J. Biol. Chem. 275:18946-18961(2000).
DR EMBL: AF252551; AAF87981.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
DR Receptor.
KW RECEPTOR.
SQ SEQUENCE 352 AA; 40293 MW; BAF8279ABAB5309 CRC64;

Query Match 83.3%; Score 935; DB 6; Length 352;
Best Local Similarity 96.7%; Pred. No. 2.5e-79;
Matches 176; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 MDYVSSPTDYIDYITSEPCOKINVKOIAARLLPPLSLVIFGVGNMVLILINCKR 60
DB 1 MDYVSSPTDYIDYITSEPCOKINVKOIAARLLPPLSLVIFGVGNMVLILINCKR 60
OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120
OY 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 180
DB 121 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 180
OY 181 HFPY 184
DB 181 HFPY 184

RESULT 11

097962 ID 097962 PRELIMINARY; PRT; 352 AA.

AC 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor type 5.
GN CCR5.
OS Pygathrix entellus (Tronkin snub-nosed monkey), and
OS Pygathrix roosei (golden snub-nosed monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=66062, 61622;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF075447; AAD19859.1;
DR EMBL: AF075444; AAD19856.1;
DR InterPro: IPR00276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
DR Receptor.
KW RECEPTOR.
SQ SEQUENCE 352 AA; 40482 MW; 037CA9E12E532F3 CRC64;

Query Match 83.3%; Score 935; DB 6; Length 352;
Best Local Similarity 95.7%; Pred. No. 2.5e-79;
Matches 176; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY 1 MDYVSSPTDYIDYITSEPCOKINVKOIAARLLPPLSLVIFGVGNMVLILINCKR 60
DB 1 MDYVSSPTDYIDYITSEPCOKINVKOIAARLLPPLSLVIFGVGNMVLILINCKR 60
OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120

OY 121 LKTDRLAVYHAFALKARTVGVVTSVITWVAFAASLPGIIFTRSQEGGLHYTCS 180
DB 121 LKTDRLAVYHAFALKARTVGVVTSVITWVAFAASLPGIIFTRSQEGGLHYTCS 180
OY 181 HFPY 184
DB 181 HFPY 184

RESULT 12

09XT14 ID 09XT14 PRELIMINARY; PRT; 352 AA.

AC 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
OC NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Spearman P.W., Mburu D.N., Graham B.S.;
RT "Differential utilization of CCR5 molecules from Three East African
RT Simian Species by the HIV-1 Envelope Glycoprotein."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF141639; AAD32684.1;
DR InterPro: IPR00276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsin.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
DR Receptor.
KW RECEPTOR.
SQ SEQUENCE 352 AA; 40550 MW; 9B078EF04D34DB36 CRC64;

Query Match 83.2%; Score 934; DB 6; Length 352;
Best Local Similarity 95.7%; Pred. No. 3.1e-79;
Matches 176; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDYVSSPTDYIDYITSEPCOKINVKOIAARLLPPLSLVIFGVGNMVLILINCKR 60
DB 1 MDYVSSPTDYIDYITSEPCOKINVKOIAARLLPPLSLVIFGVGNMVLILINCKR 60
OY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQWDFGNTMCQLLTGLYFIFGFSGIFPII 120
OY 121 LKTDRLAVYHAFALKARTVGVVTSVITWVAFAASLPGIIFTRSQEGGLHYTCS 180
DB 121 LKTDRLAVYHAFALKARTVGVVTSVITWVAFAASLPGIIFTRSQEGGLHYTCS 180
OY 181 HFPY 184
DB 181 HFPY 184

RESULT 13

095NC7 ID 095NC7 PRELIMINARY; PRT; 352 AA.

AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Nasalis larvatus (Proboscis monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Nasalis.

OX NCBI_TaxID=43780;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 phylogeny";
 RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF177882; AAK43365.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECIP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 352 AA; 40537 MW; 51FEF1486E35938E CRC64;

Query Match 83.2%; Score 934; DB 6; Length 352;
 Best Local Similarity 95.2%; Pred. No. 3.1e-79;
 Matches 177; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 OY 1 MDYVSSPTIDINVTSEPCQKINVKQIARLLPPLYSLVTFEGVGNMLVLLINCKR 60
 DB 1 MDYVSSPTIDIDYITSEPCQKINVKQIARLLPPLYSLVTFEGVGNMLVLLINCKR 60
 OY 61 LKSMTDIYLLNLAIISDLFLITVPEFAHAAQMDGNTMCOLLGLYIFGFGSIFFTI 120
 DB 61 LKSMTDIYLLNLAIISDLFLITVPEFAHAAQMDGNTMCOLLGLYIFGFGSIFFTI 120
 OY 121 LFTIDRLAVHVAHFALKARTVFGVTSVITWVAVFASLPGIIFTRSQREGIHYTCSS 180
 DB 121 LFTIDRLAVHVAHFALKARTVFGVTSVITWVAVFASLPGIIFTRSQREGIHYTCSS 180
 OY 181 HFPY 184
 DB 181 HFPY 184

RESULT 14

O95NC3 PRELIMINARY; PRT; 352 AA.
 ID O95NC3;
 AC O95NC3;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5.
 GN CCR5.
 OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Miopithecus.
 OX NCBI_TaxID=36231;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 phylogeny";
 RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF177886; AAK43369.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECIP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 352 AA; 40546 MW; 6464152F3B566AE5 CRC64;

Query Match 83.2%; Score 934; DB 6; Length 352;
 Best Local Similarity 96.2%; Pred. No. 3.1e-79;
 Matches 177; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDYVSSPTIDINVTSEPCQKINVKQIARLLPPLYSLVTFEGVGNMLVLLINCKR 60
 DB 1 MDYVSSPTIDIDYITSEPCQKINVKQIARLLPPLYSLVTFEGVGNMLVLLINCKR 60
 OY 61 LKSMTDIYLLNLAIISDLFLITVPEFAHAAQMDGNTMCOLLGLYIFGFGSIFFTI 120

DB 61 LKSMTDIYLLNLAIISDLFLITVPEFAHAAQMDGNTMCOLLGLYIFGFGSIFFTI 120
 OY 121 LFTIDRLAVHVAHFALKARTVFGVTSVITWVAVFASLPGIIFTRSQREGIHYTCSS 180
 DB 121 LFTIDRLAVHVAHFALKARTVFGVTSVITWVAVFASLPGIIFTRSQREGIHYTCSS 180
 OY 181 HFPY 184
 DB 181 HFPY 184

RESULT 15

O18770 PRELIMINARY; PRT; 352 AA.
 ID O18770;
 AC O18770;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CCR5 receptor (Fragment).
 GN CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MACC95-140A;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 Ho D.D.;
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
 DR EMBL; AF011538; AAB65738.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECIP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 352 AA; 40523 MW; 4513DB983A28ACB2 CRC64;

Query Match 83.2%; Score 933; DB 6; Length 352;
 Best Local Similarity 96.2%; Pred. No. 3.8e-79;
 Matches 177; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDYVSSPTIDINVTSEPCQKINVKQIARLLPPLYSLVTFEGVGNMLVLLINCKR 60
 DB 1 MDYVSSPTIDIDYITSEPCQKINVKQIARLLPPLYSLVTFEGVGNMLVLLINCKR 60
 OY 61 LKSMTDIYLLNLAIISDLFLITVPEFAHAAQMDGNTMCOLLGLYIFGFGSIFFTI 120
 DB 61 LKSMTDIYLLNLAIISDLFLITVPEFAHAAQMDGNTMCOLLGLYIFGFGSIFFTI 120
 OY 121 LFTIDRLAVHVAHFALKARTVFGVTSVITWVAVFASLPGIIFTRSQREGIHYTCSS 180
 DB 121 LFTIDRLAVHVAHFALKARTVFGVTSVITWVAVFASLPGIIFTRSQREGIHYTCSS 180
 OY 181 HFPY 184
 DB 181 HFPY 184

Search completed: June 3, 2003, 15:21:41
 Job time : 45.1235 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 3, 2003, 15:19:46 ; Search time 78.222 Seconds
(without alignments)
947.732 Million cell updates/sec

Title: US-09-939-226-5

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Scoring table: BLOSUM62

Searched: 1005926 seqs, 210607049 residues

Total number of hits satisfying chosen parameters: 1005926

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 08

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3: /cgn2_6/pdataa/1/paa/US07_NEW_COMB.dep.*
4: /cgn2_6/pdataa/1/paa/US08_NEW_COMB.dep.*
5: /cgn2_6/pdataa/1/paa/US09_NEW_COMB.dep.*
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7: /cgn2_6/pdataa/1/paa/US60_NEW_COMB.dep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1841	100.0	352	1	PCT-US02-29560-259	Sequence 259, App
2	1841	100.0	352	1	PCT-US02-06345-1	Sequence 1, App1
3	1841	100.0	352	1	PCT-US03-03763-1	Sequence 1, App1
4	1841	100.0	352	5	US-09-949-002-303	Sequence 303, App
5	1841	100.0	352	5	US-09-949-004-242	Sequence 242, App
6	1841	100.0	352	6	US-10-086-814-1	Sequence 1, App1
7	1841	100.0	352	6	US-10-345-882-259	Sequence 259, App
8	1841	100.0	352	6	US-10-323-314-1	Sequence 1, App1
9	1841	100.0	352	6	US-10-325-567A-352	Sequence 352, App
10	1841	100.0	352	6	US-10-290-058A-6	Sequence 6, App1
11	1841	100.0	352	6	US-10-360-828-1	Sequence 1, App1
12	1841	100.0	352	6	US-10-339-423-67	Sequence 67, App
13	1841	100.0	352	7	US-60-452-680-12568	Sequence 12568, A
14	1841	100.0	352	7	US-60-453-335-7850	Sequence 7850, Ap
15	1841	100.0	352	7	US-60-453-050-7850	Sequence 7850, Ap
16	1841	100.0	352	7	US-60-455-444-4380	Sequence 4380, Ap
17	1841	100.0	352	7	US-60-465-241-4380	Sequence 4380, Ap
18	1841	100.0	352	7	US-60-466-112-7850	Sequence 7850, Ap
19	1841	100.0	378	5	US-09-949-002-552	Sequence 552, App
20	1841	100.0	378	5	US-09-949-004-442	Sequence 442, App
21	1641.5	89.2	332	6	US-10-095-876A-2	Sequence 2, App1
22	1547	84.0	334	6	US-10-219-051B-10290	Sequence 10290, A
23	1547	84.0	354	6	US-10-219-051B-10294	Sequence 10294, A
24	1364	74.1	350	6	US-10-225-567A-460	Sequence 460, App
25	1364	74.1	360	6	US-10-239-423-64	Sequence 64, App
26	1364	74.1	360	7	US-60-452-680-12372	Sequence 12372, A

27	1364	74.1	360	7	US-60-453-135-7700	Sequence 7700, Ap
28	1364	74.1	360	7	US-60-453-050-7700	Sequence 7700, Ap
29	1364	74.1	360	7	US-60-455-444-4289	Sequence 4289, Ap
30	1364	74.1	360	7	US-60-456-241-4289	Sequence 4289, Ap
31	1364	74.1	360	7	US-60-466-412-7700	Sequence 7700, Ap
32	1364	74.1	360	7	US-09-949-004-443	Sequence 443, App
33	1364	74.1	377	5	US-09-949-016-11221	Sequence 11221, Ap
34	1364	74.1	268	6	US-10-160-619-164	Sequence 164, App
35	1335	72.5	268	6	US-09-893-512A-14	Sequence 162, App
36	1283.5	69.7	384	5	US-09-893-004-244	Sequence 14, App
37	1224	66.5	374	5	US-09-893-512A-13	Sequence 244, App
38	1224	66.5	374	5	US-10-239-423-63	Sequence 13, App
39	1224	66.5	374	6	US-10-215-051B-10292	Sequence 63, App
40	1224	66.5	374	6	US-10-215-051B-10296	Sequence 10292, App
41	1224	66.5	374	6	US-60-453-680-12373	Sequence 10296, App
42	1224	66.5	374	7	US-60-453-135-7701	Sequence 12373, A
43	1224	66.5	374	7	US-60-453-050-7701	Sequence 7701, App
44	1224	66.5	374	7	US-60-455-444-4290	Sequence 7701, App
45	1224	66.5	374	7	US-60-455-444-4290	Sequence 4290, App

ALIGNMENTS

RESULT 1
PCT-US02-29560-259

```

; Sequence 259, Application PC/TUS02295600
; GENERAL INFORMATION:

```

APPLICANT: Alar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Hervez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnick, Albert
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FIELD OF INVENTION

```

? FILE REFERENCE: 018301-002/10PC
? CURRENT APPLICATION NUMBER: PCT/US02/29560
? CURRENT FILING DATE: 2025-11-01
? PRIOR APPLICATION NUMBER: US 60/323,469
? PRIOR FILING DATE: 2001-09-17
? NUMBER OF SEQ ID NOS: 412
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 259
? LENGTH: 352
? TYPE: PRT
? ORGANISM: Homo sapiens
PCT-US02-29560-259

Query Match          100.0%; Score 1841; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Qy	1	1MJOVSSPIYDINYYTSEPCOKINVKQIAARLLPPLVSLVPIFGFVGMLVILLINCKR	60
Db	1	1MJOYSSPIYDINYYTSEPCOKINVKQIAARLLPPLVSLVPIFGFVGMLVILLINCKR	60
Qy	61	1KSMDDIYLNTAISDLFFLLTVFPWMAHYAAAQMDFGNTMCOLLTGLYFTGFSGIPIIT	120
Db	61	1KSMDDIYLNTAISDLFFLLTVFPWMAHYAAAQMDFGNTMCOLLTGLYFTGFSGIPIIT	120
Qy	121	1LTIDRBYLVNAVAEVALRKARFTPECVMTSVITWVAVASLPGIITFRSQEGHLYPCSS	180
Db	121	1LTIDRBYLVNAVAEVALRKARFTPECVMTSVITWVAVASLPGIITFRSQEGHLYPCSS	180
Qy	181	1HPFYSQYQPMKNFOTLKIVLGLVLPPLVMNYICSGILKTLLRCRNEKKRRHRAVRLFTI	240
Db	181	1HPFYSQYQPMKNFOTLKIVLGLVLPPLVMNYICSGILKTLLRCRNEKKRRHRAVRLFTI	240
Qy	241	1MYVFLFMAPIYIVLLNTPOEFBLNCCSSNRRLDQAMQVETFLGATHCCINPIITAYV	300

Db 241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLTGTHCCINPIIYAFV 300
QY 301 GEFERNYLLVFQKHIAKRFCKCISIFOEAPERASSVYTRSTGEDEISVGL 352
Db 301 GEFERNYLLVFQKHIAKRFCKCISIFOEAPERASSVYTRSTGEDEISVGL 352

RESULT 2
PCT-US02-06345-1
Sequence 1, Application PC/TUS0206345
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc., et al.
TITLE OF INVENTION: Sulfated CCR5 Peptides for HIV-1 Infection
FILE REFERENCE: 61010-AB1-PCT/JPM/JTL
CURRENT APPLICATION NUMBER: PCT/US02/06345
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 1
LENGTH: 352
TYPE: PRT
ORGANISM: Human
PCT-US02-06345-1

Query Match 100.0%; Score 1841; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCOKINVKQIARLLPPLYSVFTFGVGNMLVILLINCR 60
Db 1 MDYVSSPIYDINNTYSEPCOKINVKQIARLLPPLYSVFTFGVGNMLVILLINCR 60
QY 61 LKSMIDIYLLNLAISDLFFLLVPPFWAHYAAAQMDPGNTMQLTGLYFIFGFSGIFETI 120
Db 61 LKSMIDIYLLNLAISDLFFLLVPPFWAHYAAAQMDPGNTMQLTGLYFIFGFSGIFETI 120
QY 121 LITIDRYLAVVAHVAFLAKARVTFGVVSVITWVAVFAASLPGIIFTRSQKGLHYTCSS 180
Db 121 LITIDRYLAVVAHVAFLAKARVTFGVVSVITWVAVFAASLPGIIFTRSQKGLHYTCSS 180
QY 181 HEPYSOYQFWKMFQTLKIYILGLVPLVMVTCYSGLTKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HEPYSOYQFWKMFQTLKIYILGLVPLVMVTCYSGLTKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLTGTHCCINPIIYAFV 300
Db 241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLTGTHCCINPIIYAFV 300
QY 301 GEFERNYLLVFQKHIAKRFCKCISIFOEAPERASSVYTRSTGEDEISVGL 352
Db 301 GEFERNYLLVFQKHIAKRFCKCISIFOEAPERASSVYTRSTGEDEISVGL 352

RESULT 3
PCT-US03-03763-1
Sequence 1, Application PC/TUS0303763
GENERAL INFORMATION:
APPLICANT: Hua, Shaobing
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TITLE OF INVENTION: METHODS FOR GENERATING ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-728
CURRENT APPLICATION NUMBER: PCT/US03/03763
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/071,866
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133,978
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1

LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-03763-1

Query Match 100.0%; Score 1841; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCOKINVKQIARLLPPLYSVFTFGVGNMLVILLINCR 60
Db 1 MDYVSSPIYDINNTYSEPCOKINVKQIARLLPPLYSVFTFGVGNMLVILLINCR 60
QY 61 LKSMIDIYLLNLAISDLFFLLVPPFWAHYAAAQMDPGNTMQLTGLYFIFGFSGIFETI 120
Db 61 LKSMIDIYLLNLAISDLFFLLVPPFWAHYAAAQMDPGNTMQLTGLYFIFGFSGIFETI 120
QY 121 LITIDRYLAVVAHVAFLAKARVTFGVVSVITWVAVFAASLPGIIFTRSQKGLHYTCSS 180
Db 121 LITIDRYLAVVAHVAFLAKARVTFGVVSVITWVAVFAASLPGIIFTRSQKGLHYTCSS 180
QY 181 HEPYSOYQFWKMFQTLKIYILGLVPLVMVTCYSGLTKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HEPYSOYQFWKMFQTLKIYILGLVPLVMVTCYSGLTKTLRCRNEKRRHRAVRLIFTI 240
QY 241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLTGTHCCINPIIYAFV 300
Db 241 MIVYFLFMAPYNIIVLLNTFOEFFGLNCCSSNRDLQAMQVETLTGTHCCINPIIYAFV 300
QY 301 GEFERNYLLVFQKHIAKRFCKCISIFOEAPERASSVYTRSTGEDEISVGL 352
Db 301 GEFERNYLLVFQKHIAKRFCKCISIFOEAPERASSVYTRSTGEDEISVGL 352

RESULT 4
US-09-949-002-303
Sequence 303, Application US/09949002
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 303
LENGTH: 352
TYPE: PRT
ORGANISM: Human
US-09-949-002-303

Query Match 100.0%; Score 1841; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCOKINVKQIARLLPPLYSVFTFGVGNMLVILLINCR 60
Db 1 MDYVSSPIYDINNTYSEPCOKINVKQIARLLPPLYSVFTFGVGNMLVILLINCR 60
QY 61 LKSMIDIYLLNLAISDLFFLLVPPFWAHYAAAQMDPGNTMQLTGLYFIFGFSGIFETI 120
Db 61 LKSMIDIYLLNLAISDLFFLLVPPFWAHYAAAQMDPGNTMQLTGLYFIFGFSGIFETI 120
QY 121 LITIDRYLAVVAHVAFLAKARVTFGVVSVITWVAVFAASLPGIIFTRSQKGLHYTCSS 180
Db 121 LITIDRYLAVVAHVAFLAKARVTFGVVSVITWVAVFAASLPGIIFTRSQKGLHYTCSS 180
QY 181 HEPYSOYQFWKMFQTLKIYILGLVPLVMVTCYSGLTKTLRCRNEKRRHRAVRLIFTI 240
Db 181 HEPYSOYQFWKMFQTLKIYILGLVPLVMVTCYSGLTKTLRCRNEKRRHRAVRLIFTI 240

Db 181 HEPYSOYOFMKNPOTLKIIVILGLVPLPLVMYICYSGLIKTLRCRNEKKRRRAVRLFTI 240
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1
Query Match 100.0%; Score 1841; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2,5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-09-949-004-242
RESULT 5
US-09-949-004-242
; Sequence 242, Application US/0949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00848
; CURRENT APPLICATION NUMBER: US/09/949,004
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 242
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Human
US-09-949-004-242
Query Match 100.0%; Score 1841; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2,5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-086-814-1
RESULT 6
US-10-086-814-1
; Sequence 1, Application US/10086814
; GENERAL INFORMATION:
; APPLICANT: Draglic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SOLICATED CCNS PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatenSeq for Windows Version 3.1

Db 241 MIVFLEWAPYNIYLLNTFOEPFGLNCCSSNRLDQAMQVETLGMTHCCINPIYAFV 300
Db 241 MIVFLEWAPYNIYLLNTFOEPFGLNCCSSNRLDQAMQVETLGMTHCCINPIYAFV 300
Qy 301 GEFKRNLYLVFQKHIAKRFCKCSIFQOEAPEBASVYTRSTGEDEISVGL 352
Db 301 GEFKRNLYLVFQKHIAKRFCKCSIFQOEAPEBASVYTRSTGEDEISVGL 352
US-10-086-814-1
Query Match 100.0%; Score 1841; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2,5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-245-882-259
RESULT 7
US-10-245-882-259
; Sequence 259, Application US/10245882
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Glash, Kurt C.
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-002710US
; CURRENT APPLICATION NUMBER: US/10/245,882
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/323,887
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/325,114
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/340,944
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/355,145
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/355,257
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/369,899
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 259

LENGTH: 352
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-245-882-259

Query Match 100.0%; Score 1841; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.5e-171;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINITYSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
 QY 61 LKSMIDYLLNLAISDLFELLVPPFAHAAQWMDGNTMQLLGLYFIFGSSGIFPII 120
 DB 61 LKSMIDYLLNLAISDLFELLVPPFAHAAQWMDGNTMQLLGLYFIFGSSGIFPII 120
 QY 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAFAVSLPGIIFTSQKGLHYTCSS 180
 DB 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAFAVSLPGIIFTSQKGLHYTCSS 180
 QY 181 HPPYSOYQFWMKFOQLKIYILGLVPLVMVICYGIIKTLRCNKKRRRAVRLIFTI 240
 DB 181 HPPYSOYQFWMKFOQLKIYILGLVPLVMVICYGIIKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIYVFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
 DB 241 MIYVFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
 QY 301 GEKFRNYLLVFFOKHIAKRCCKCSIFQOEAPEERASSVYTRSTGEOEISVGL 352
 DB 301 GEKFRNYLLVFFOKHIAKRCCKCSIFQOEAPEERASSVYTRSTGEOEISVGL 352

RESULT 8

US-10-323-314-1
 Sequence 1, Application US/10323314
 GENERAL INFORMATION:
 APPLICANT: Dragic, Tatjana
 APPLICANT: Olson, William
 TITLE OF INVENTION: SOLIDATED CCR5 PEPTIDES FOR HIV-1 INFECTION
 FILE REFERENCE: 2048/61010-1/JPW/MAF/DJK
 CURRENT APPLICATION NUMBER: US/10/323,314
 CURRENT FILING DATE: 2002-12-19
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1
 LENGTH: 352
 TYPE: PRT
 ORGANISM: human
 US-10-323-314-1

Query Match 100.0%; Score 1841; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.5e-171;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINITYSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
 QY 61 LKSMIDYLLNLAISDLFELLVPPFAHAAQWMDGNTMQLLGLYFIFGSSGIFPII 120
 DB 61 LKSMIDYLLNLAISDLFELLVPPFAHAAQWMDGNTMQLLGLYFIFGSSGIFPII 120
 QY 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAFAVSLPGIIFTSQKGLHYTCSS 180
 DB 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAFAVSLPGIIFTSQKGLHYTCSS 180
 QY 181 HPPYSOYQFWMKFOQLKIYILGLVPLVMVICYGIIKTLRCNKKRRRAVRLIFTI 240
 DB 181 HPPYSOYQFWMKFOQLKIYILGLVPLVMVICYGIIKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIYVFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
 DB 241 MIYVFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300

DB 241 MIYVFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
 QY 301 GEKFRNYLLVFFOKHIAKRCCKCSIFQOEAPEERASSVYTRSTGEOEISVGL 352
 DB 301 GEKFRNYLLVFFOKHIAKRCCKCSIFQOEAPEERASSVYTRSTGEOEISVGL 352

RESULT 9

US-10-225-567A-352
 Sequence 352, Application US/10225567A
 GENERAL INFORMATION:
 APPLICANT: Lifespan Biosciences
 APPLICANT: Brown, Joseph P.
 APPLICANT: Burner, Glenna C.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 352
 LENGTH: 352
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-225-567A-352

Query Match 100.0%; Score 1841; DB 6; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.5e-171;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINITYSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINITYSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
 QY 61 LKSMIDYLLNLAISDLFELLVPPFAHAAQWMDGNTMQLLGLYFIFGSSGIFPII 120
 DB 61 LKSMIDYLLNLAISDLFELLVPPFAHAAQWMDGNTMQLLGLYFIFGSSGIFPII 120
 QY 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAFAVSLPGIIFTSQKGLHYTCSS 180
 DB 121 LTTIDRYLAHVAVFALKARVTFGVVSVITWVAFAVSLPGIIFTSQKGLHYTCSS 180
 QY 181 HPPYSOYQFWMKFOQLKIYILGLVPLVMVICYGIIKTLRCNKKRRRAVRLIFTI 240
 DB 181 HPPYSOYQFWMKFOQLKIYILGLVPLVMVICYGIIKTLRCNKKRRRAVRLIFTI 240
 QY 241 MIYVFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
 DB 241 MIYVFLFMAPYINIVILLNTFOEFFGLNCCSSNRDLQAMQVETLGMTHCCINPIITAFV 300
 QY 301 GEKFRNYLLVFFOKHIAKRCCKCSIFQOEAPEERASSVYTRSTGEOEISVGL 352
 DB 301 GEKFRNYLLVFFOKHIAKRCCKCSIFQOEAPEERASSVYTRSTGEOEISVGL 352

RESULT 10

US-10-290-058A-6
 Sequence 6, Application US/10290058A
 GENERAL INFORMATION:
 APPLICANT: Siles-Santlago, Immaculada
 TITLE OF INVENTION: Urological Disorders and Compositions for Treating
 FILE REFERENCE: MP101-2891RM
 CURRENT APPLICATION NUMBER: US/10/290,058A
 CURRENT FILING DATE: 2002-11-07
 PRIOR APPLICATION NUMBER: 60/344,552
 PRIOR FILING DATE: 2001-11-07
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6
LENGTH: 352
TYPE: PRT
ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match 100.0%; Score 1841; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVIFGFVGMVLVILINCKR 60
DB 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVIFGFVGMVLVILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFPII 120
QY 121 LITDRILAVVHAVALKARTVTFGVTSVITVVAVFASLPGLIIFRSQEGHLHYTCS 180
DB 121 LITDRILAVVHAVALKARTVTFGVTSVITVVAVFASLPGLIIFRSQEGHLHYTCS 180
QY 181 HEPYSOYQFMKNFOTLIVILGLVPLLVWVICYSGILKTLRCRNEKKRRRAVRLFTI 240
DB 181 HEPYSOYQFMKNFOTLIVILGLVPLLVWVICYSGILKTLRCRNEKKRRRAVRLFTI 240
QY 241 MIYFLFMAPYNIYLLNTFOEFGNLNCSNNRLDQAMQVETLGHHCINPIIYAFV 300
DB 241 MIYFLFMAPYNIYLLNTFOEFGNLNCSNNRLDQAMQVETLGHHCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 11

US-10-360-828-1
Sequence 1, Application US/10360828
GENERAL INFORMATION:
APPLICANT: Hua, Shaoling
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727
CURRENT APPLICATION NUMBER: US/10/360, 828
PRIOR FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/071, 866
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/072, 301
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 10/133, 978
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-360-828-1

Query Match 100.0%; Score 1841; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVIFGFVGMVLVILINCKR 60
DB 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVIFGFVGMVLVILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFPII 120
QY 121 LITDRILAVVHAVALKARTVTFGVTSVITVVAVFASLPGLIIFRSQEGHLHYTCS 180

DB 121 LITDRILAVVHAVALKARTVTFGVTSVITVVAVFASLPGLIIFRSQEGHLHYTCS 180
QY 181 HEPYSOYQFMKNFOTLIVILGLVPLLVWVICYSGILKTLRCRNEKKRRRAVRLFTI 240
DB 181 HEPYSOYQFMKNFOTLIVILGLVPLLVWVICYSGILKTLRCRNEKKRRRAVRLFTI 240
QY 241 MIYFLFMAPYNIYLLNTFOEFGNLNCSNNRLDQAMQVETLGHHCINPIIYAFV 300
DB 241 MIYFLFMAPYNIYLLNTFOEFGNLNCSNNRLDQAMQVETLGHHCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 12

US-10-239-423-67
Sequence 67, Application US/10239423
GENERAL INFORMATION:
APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239, 423
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: DE10016013.1
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 67
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67

Query Match 100.0%; Score 1841; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-171;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVIFGFVGMVLVILINCKR 60
DB 1 MDYOVSSPIYDINYYTSEPCOKINVKQIAARLLPPLYSLVIFGFVGMVLVILINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFSGIFPII 120
QY 121 LITDRILAVVHAVALKARTVTFGVTSVITVVAVFASLPGLIIFRSQEGHLHYTCS 180
DB 121 LITDRILAVVHAVALKARTVTFGVTSVITVVAVFASLPGLIIFRSQEGHLHYTCS 180
QY 181 HEPYSOYQFMKNFOTLIVILGLVPLLVWVICYSGILKTLRCRNEKKRRRAVRLFTI 240
DB 181 HEPYSOYQFMKNFOTLIVILGLVPLLVWVICYSGILKTLRCRNEKKRRRAVRLFTI 240
QY 241 MIYFLFMAPYNIYLLNTFOEFGNLNCSNNRLDQAMQVETLGHHCINPIIYAFV 300
DB 241 MIYFLFMAPYNIYLLNTFOEFGNLNCSNNRLDQAMQVETLGHHCINPIIYAFV 300
QY 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352
DB 301 GEKFRNLLVFFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGEQISVGL 352

RESULT 13

US-60-453-680-12568
 ; Sequence 12568, Application US/60452680
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: GRUBE, Andrew
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001450
 ; CURRENT APPLICATION NUMBER: US/60/452,680
 ; CURRENT FILING DATE: 2003-03-07
 ; NUMBER OF SEQ ID NOS: 116213
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 12568
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-453-680-12568

Query Match 100.0%; Score 1841; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.5e-171;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCOKINVKQIAARLLPPLYSIVTFGFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINNTYSEPCOKINVKQIAARLLPPLYSIVTFGFGVGNMLVILLINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAAQMDFGNTMQLTGLYTFGFGSIFPFI 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAAQMDFGNTMQLTGLYTFGFGSIFPFI 120
 QY 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 DB 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 QY 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 DB 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 QY 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 DB 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 QY 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 DB 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 QY 241 MIYFLFWAPYNIYVLLNTFOEFFGLNCCSSNRDQAOVETLGMTHCCINPIIYAFV 300
 DB 241 MIYFLFWAPYNIYVLLNTFOEFFGLNCCSSNRDQAOVETLGMTHCCINPIIYAFV 300
 QY 301 GEKFRNLYLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352
 DB 301 GEKFRNLYLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352

RESULT 14
 US-60-453-135-7850
 ; Sequence 7850, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKUBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001456
 ; CURRENT APPLICATION NUMBER: US/60/453,135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 7850
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-453-135-7850

Query Match 100.0%; Score 1841; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.5e-171;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCOKINVKQIAARLLPPLYSIVTFGFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINNTYSEPCOKINVKQIAARLLPPLYSIVTFGFGVGNMLVILLINCKR 60

QY 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAAQMDFGNTMQLTGLYTFGFGSIFPFI 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAAQMDFGNTMQLTGLYTFGFGSIFPFI 120
 QY 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 DB 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 QY 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 DB 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 QY 241 MIYFLFWAPYNIYVLLNTFOEFFGLNCCSSNRDQAOVETLGMTHCCINPIIYAFV 300
 DB 241 MIYFLFWAPYNIYVLLNTFOEFFGLNCCSSNRDQAOVETLGMTHCCINPIIYAFV 300
 QY 301 GEKFRNLYLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352
 DB 301 GEKFRNLYLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352

RESULT 15
 US-60-453-050-7850
 ; Sequence 7850, Application US/60453050
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: LUKE, May
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001457
 ; CURRENT APPLICATION NUMBER: US/60/453,050
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 7850
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-453-050-7850

Query Match 100.0%; Score 1841; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.5e-171;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINNTYSEPCOKINVKQIAARLLPPLYSIVTFGFGVGNMLVILLINCKR 60
 DB 1 MDYVSSPIYDINNTYSEPCOKINVKQIAARLLPPLYSIVTFGFGVGNMLVILLINCKR 60
 QY 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAAQMDFGNTMQLTGLYTFGFGSIFPFI 120
 DB 61 LKSMTDIYLLNLAIISDLFFLLTPFWAHYAAAQMDFGNTMQLTGLYTFGFGSIFPFI 120
 QY 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 DB 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 QY 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 DB 121 LTTIDRYLAVNAHVAFLKARTVFGVTSVITWVAVASLPGIIFTRSQEGHLYTCS 180
 QY 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 DB 181 HFPYSOYQFWKNEQTLKIVILGLVPLVAVICYSGLTKTLRCNEKKRRHRAVLIPTI 240
 QY 241 MIYFLFWAPYNIYVLLNTFOEFFGLNCCSSNRDQAOVETLGMTHCCINPIIYAFV 300
 DB 241 MIYFLFWAPYNIYVLLNTFOEFFGLNCCSSNRDQAOVETLGMTHCCINPIIYAFV 300
 QY 301 GEKFRNLYLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352
 DB 301 GEKFRNLYLVFQKHIAKRCCKCSIFQOEAPERASSVYTRSTGDEISVGL 352

Search completed: June 3, 2003, 15:33:14
 Job time : 80.2222 secs

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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:19:11 ; Search time 170.635 Seconds

(Without alignments)
812.364 Million cell updates/sec

Title: US-09-939-226-6

Perfect score: 1122
Sequence: 1 MDYQVSSPIVDINVTSEPC.....AACHGILLGNPKNSASVSK 215Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/PCRU5_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1122	100.0	215	20	US-09-626-500-6
2	1122	100.0	215	20	US-09-626-939-6
3	1122	100.0	215	23	US-09-938-703-6
4	1122	100.0	215	23	US-09-938-719-6
5	1122	100.0	215	23	US-09-939-226-6
6	969.5	86.4	191	27	US-60-182-562-1416

	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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	958	85.4	184	20	US-09-626-939-4	Sequence 4, Appl1																																	
	958	85.4	184	23	US-09-938-703-4	Sequence 4, Appl1																																	
	958	85.4	184	23	US-09-938-719-4	Sequence 4, Appl1																																	
	958	85.4	184	23	US-09-939-226-4	Sequence 4, Appl1																																	
	958	85.4	352	1	PCT-US01-04152A-22	Sequence 22, Appl1																																	
	958	85.4	352	1	PCT-US01-04153A-22	Sequence 22, Appl1																																	
	958	85.4	352	1	PCT-US01-06699-1	Sequence 22, Appl1																																	
	958	85.4	352	1	PCT-US01-10708-3	Sequence 22, Appl1																																	
	958	85.4	352	1	PCT-US02-03634-22	Sequence 22, Appl1																																	
	958	85.4	352	10	US-08-661-393-2	Sequence 2, Appl1																																	
	958	85.4	352	11	US-08-771-276-2	Sequence 2, Appl1																																	
	958	85.4	352	12	US-08-864-458-4	Sequence 4, Appl1																																	
	958	85.4	352	15	US-09-195-662A-2	Sequence 2, Appl1																																	
	958	85.4	352	17	US-09-339-912A-2	Sequence 2, Appl1																																	
	958	85.4	352	19	US-09-502-783A-2	Sequence 2, Appl1																																	
	958	85.4	352	19	US-09-502-784A-2	Sequence 2, Appl1																																	
	958	85.4	352	20	US-09-626-500-5	Sequence 5, Appl1																																	
	958	85.4	352	20	US-09-626-939-5	Sequence 5, Appl1																																	
	958	85.4	352	21	US-09-725-285-2	Sequence 2, Appl1																																	
	958	85.4	352	21	US-09-724-221A-14	Sequence 14, Appl1																																	
	958	85.4	352	21	US-09-759-841-2	Sequence 2, Appl1																																	
	958	85.4	352	21	US-09-779-879A-22	Sequence 22, Appl1																																	
	958	85.4	352	21	US-09-779-880A-22	Sequence 22, Appl1																																	
	958	85.4	352	21	US-09-796-202-1	Sequence 1, Appl1																																	
	958	85.4	352	22	US-09-813-653-15	Sequence 15, Appl1																																	
	958	85.4	352	22	US-09-866-509-477	Sequence 477, Appl1																																	
	958	85.4	352	23	US-09-938-703-5	Sequence 5, Appl1																																	
	958	85.4	352	23	US-09-939-226-5	Sequence 5, Appl1																																	
	958	85.4	352	24	US-10-067-800-22	Sequence 22, Appl1																																	
	958	85.4	352	24	US-10-071-866-1	Sequence 1, Appl1																																	
	958	85.4	352	24	US-10-072-301-1	Sequence 1, Appl1																																	
	958	85.4	352	25	US-10-106-632-2	Sequence 2, Appl1																																	
	958	85.4	352	25	US-10-133-978-1	Sequence 1, Appl1																																	
	958	85.4	352	25	US-10-135-839-12	Sequence 12, Appl1																																	
	958	85.4	352	26	US-10-232-686-2	Sequence 2, Appl1																																	
	958	85.4	309	27	US-60-229-515-844	Sequence 844, Appl1																																	
	953	84.9	352	12	US-08-864-458-2	Sequence 2, Appl1																																	

ALIGNMENTS

RESULT 1
US-09-626-500-6
Sequence 6, Application US/09626500

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/626,500
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/633,752

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 6:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-626-500-6

Query Match 100.0%; Score 1122; DB 20; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINVTSEPCOKINVKQIARLLPPLYSLVETFGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINVTSEPCOKINVKQIARLLPPLYSLVETFGVGNMLVILLINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFEFLTPVFWAHYAAAQMDFGNTMCOLLTGLYFIFGFSGIFPFI 120
DB 61 LKSMTDIYLLNLAIISDLFEFLTPVFWAHYAAAQMDFGNTMCOLLTGLYFIFGFSGIFPFI 120
QY 121 LTTIDRYLAIVAAVPAALAKRTVFGVTVSVITWVAVAFASLPGLIIFTRSKRGHLYTCSS 180
DB 121 LTTIDRYLAIVAAVPAALAKRTVFGVTVSVITWVAVAFASLPGLIIFTRSKRGHLYTCSS 180
QY 181 HFPYIKDSHLGAGPAAACHGHLILGNPKNSASYSK 215
DB 181 HFPYIKDSHLGAGPAAACHGHLILGNPKNSASYSK 215

RESULT 2
US-09-626-939-6
Sequence 6, Application US/09626939
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARENTIER, MARC
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodde, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/626,939
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,752
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-626-939-6

Query Match 100.0%; Score 1122; DB 20; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINVTSEPCOKINVKQIARLLPPLYSLVETFGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINVTSEPCOKINVKQIARLLPPLYSLVETFGVGNMLVILLINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFEFLTPVFWAHYAAAQMDFGNTMCOLLTGLYFIFGFSGIFPFI 120
DB 61 LKSMTDIYLLNLAIISDLFEFLTPVFWAHYAAAQMDFGNTMCOLLTGLYFIFGFSGIFPFI 120
QY 121 LTTIDRYLAIVAAVPAALAKRTVFGVTVSVITWVAVAFASLPGLIIFTRSKRGHLYTCSS 180
DB 121 LTTIDRYLAIVAAVPAALAKRTVFGVTVSVITWVAVAFASLPGLIIFTRSKRGHLYTCSS 180
QY 181 HFPYIKDSHLGAGPAAACHGHLILGNPKNSASYSK 215
DB 181 HFPYIKDSHLGAGPAAACHGHLILGNPKNSASYSK 215

RESULT 3
US-09-938-703-6
Sequence 6, Application US/09938703
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARENTIER, MARC
APPLICANT: VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodde, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

Query Match 100.0%; Score 1122; DB 23; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINVTSEPCOKINVKQIARLLPPLYSLVETFGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINVTSEPCOKINVKQIARLLPPLYSLVETFGVGNMLVILLINCKR 60

Db 1 MDYVSSPIYDINTYTSPECOKINVKOIAARLLPPLYSLVIFSGVGNMVLILLINCR 60
Qy 61 LKSMTDIYLLNLAISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYIFGFSGIEFI 120
Db 61 LKSMTDIYLLNLAISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYIFGFSGIEFI 120
Qy 121 LITDRILAVVHAVALKARTVTGVTSTVTTWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LITDRILAVVHAVALKARTVTGVTSTVTTWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HFPYIKDHLGAGPAACHGHLILGNPNKSASVSK 215
Db 181 HFPYIKDHLGAGPAACHGHLILGNPNKSASVSK 215

RESULT 4
US-09-938-719-6
Sequence 6, Application US/09938719
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

Query Match 100.0%; Score 1122; DB 23; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 HFPYIKDHLGAGPAACHGHLILGNPNKSASVSK 215
Db 181 HFPYIKDHLGAGPAACHGHLILGNPNKSASVSK 215

RESULT 5
US-09-939-226-6
Sequence 6, Application US/09939226
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6

Query Match 100.0%; Score 1122; DB 23; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYVSSPIYDINTYTSPECOKINVKOIAARLLPPLYSLVIFSGVGNMVLILLINCR 60
Db 1 MDYVSSPIYDINTYTSPECOKINVKOIAARLLPPLYSLVIFSGVGNMVLILLINCR 60
Qy 61 LKSMTDIYLLNLAISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYIFGFSGIEFI 120
Db 61 LKSMTDIYLLNLAISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYIFGFSGIEFI 120
Qy 121 LITDRILAVVHAVALKARTVTGVTSTVTTWVAVFASLPGIIFTRSQEGLHYTCSS 180
Db 121 LITDRILAVVHAVALKARTVTGVTSTVTTWVAVFASLPGIIFTRSQEGLHYTCSS 180
Qy 181 HFPYIKDHLGAGPAACHGHLILGNPNKSASVSK 215
Db 181 HFPYIKDHLGAGPAACHGHLILGNPNKSASVSK 215

RESULT 6
US-60-182-562-1416
Sequence 1416, Application US/60182562

GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000247
CURRENT APPLICATION NUMBER: US/60/182,562
CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 1658
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1416
LENGTH: 191
TYPE: PRT
ORGANISM: HUMAN
US-60-182-562-1416

Query Match 86.4%; Score 969.5; DB 27; Length 191;
Best Local Similarity 99.0%; Pred. No. 2.4e-88;
Matches 189; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 26 KQIARLPPLYSVFIFGVGMVLLILNCKRLKSMTDIYLLMLAISDLFFLLTFP 85
DB 1 KQIARLPPLYSVFIFGVGMVLLILNCKRLKSMTDIYLLMLAISDLFFLLTFP 60

QY 86 MAHYAAQMDFGNTMQLLTGLYFIFGFSGIFELLITDRYLAVVAVFALKARTVTEG 145
DB 61 MAHYAAQMDFGNTMQLLTGLYFIFGFSGIFELLITDRYLAVVAVFALKARTVTEG 120

QY 146 VVTSVITWVAVFASLPGLIFTRSQKGLHYTCSSHPY-INDSHGAPPAACHHLL 204
DB 121 VVTSVITWVAVFASLPGLIFTRSQKGLHYTCSSHPYINDSHGAPPAACHHLL 180

QY 205 GNPKNASYSK 215
DB 181 GNPKNASYSK 191

RESULT 7
US-09-626-500-4
Sequence 4, Application US/09626500
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodbe, Martens, Olsson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/626,500
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,752
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-626-500-4

Query Match 85.4%; Score 958; DB 20; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINYYISECCQKINQIARLLPLYSVFIFGVGMVLLILNCKR 60
DB 1 MDYVSSPIYDINYYISECCQKINQIARLLPLYSVFIFGVGMVLLILNCKR 60

QY 61 LKSMTDIYLLMLAISDLFFLLTFPEWAAHYAAQMDFGNTMQLLTGLYFIFGFSGIFELI 120
DB 61 LKSMTDIYLLMLAISDLFFLLTFPEWAAHYAAQMDFGNTMQLLTGLYFIFGFSGIFELI 120

QY 121 LITDRYLAVVAVFALKARTVTEGVTSVITWVAVFASLPGLIFTRSQKGLHYTCSS 180
DB 121 LITDRYLAVVAVFALKARTVTEGVTSVITWVAVFASLPGLIFTRSQKGLHYTCSS 180

QY 181 HEPY 184
DB 181 HEPY 184

RESULT 8
US-09-626-939-4
Sequence 4, Application US/09626939
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodbe, Martens, Olsson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/626,939
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,752
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-626-939-4

Query Match 85.4%; Score 958; DB 20; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINTYSEPCOKINVKOIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
DB 1 MDYOVSSPIYDINTYSEPCOKINVKOIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTVPMVAHYAAQMDPGNTMQLTGLYFIKFGSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPMVAHYAAQMDPGNTMQLTGLYFIKFGSGIFPII 120
QY 121 LTTIDRLAVVAHVAFALKARTVTFGVVTSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
DB 121 LTTIDRLAVVAHVAFALKARTVTFGVVTSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
QY 181 HFPY 184
DB 181 HFPY 184

RESULT 9
US-09-938-703-4
Sequence 4, Application US/09938703
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

Query Match 85.4%; Score 958; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINTYSEPCOKINVKOIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
DB 1 MDYOVSSPIYDINTYSEPCOKINVKOIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTVPMVAHYAAQMDPGNTMQLTGLYFIKFGSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPMVAHYAAQMDPGNTMQLTGLYFIKFGSGIFPII 120
QY 121 LTTIDRLAVVAHVAFALKARTVTFGVVTSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
DB 121 LTTIDRLAVVAHVAFALKARTVTFGVVTSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180

DB 121 LTTIDRLAVVAHVAFALKARTVTFGVVTSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
QY 181 HFPY 184
DB 181 HFPY 184

RESULT 10
US-09-938-719-4
Sequence 4, Application US/09938719
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4

Query Match 85.4%; Score 958; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINTYSEPCOKINVKOIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
DB 1 MDYOVSSPIYDINTYSEPCOKINVKOIAARLLPPLYSLVFIKFGVGNMLVILLINCKR 60
QY 61 LKSMTDIYLLNLAIISDLFFLLTVPMVAHYAAQMDPGNTMQLTGLYFIKFGSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTVPMVAHYAAQMDPGNTMQLTGLYFIKFGSGIFPII 120
QY 121 LTTIDRLAVVAHVAFALKARTVTFGVVTSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
DB 121 LTTIDRLAVVAHVAFALKARTVTFGVVTSVITWVAVAFASLPGIITFRSQKGLHYTCSS 180
QY 181 HFPY 184
DB 181 HFPY 184

RESULT 11

US-09-939-226-4
; Sequence 4, Application US/09939226
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4
Query Match 85.4%; Score 958; DB 23; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYOVSSPIYDINVTSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
DB 1 MDYOVSSPIYDINVTSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
QY 61 LKSMIDIVLNLAIISDLFFLLVPPFAHAAQMDPGNTMCGLLTGLYIFGFSGIFETI 120
DB 61 LKSMIDIVLNLAIISDLFFLLVPPFAHAAQMDPGNTMCGLLTGLYIFGFSGIFETI 120
QY 121 LITIDRYLAHVAVFALKARVTFEGVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
DB 121 LITIDRYLAHVAVFALKARVTFEGVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
QY 181 HPPY 184
DB 181 HPPY 184

RESULT 12

PCT-US01-04152A-22
; Sequence 22, Application PC/TUS0104152A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10

; FILE REFERENCE: 1488.115PCOB
; CURRENT APPLICATION NUMBER: PCT/US01/04152A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-04152A-22

Query Match 85.4%; Score 958; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.7e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINVTSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
DB 1 MDYOVSSPIYDINVTSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
QY 61 LKSMIDIVLNLAIISDLFFLLVPPFAHAAQMDPGNTMCGLLTGLYIFGFSGIFETI 120
DB 61 LKSMIDIVLNLAIISDLFFLLVPPFAHAAQMDPGNTMCGLLTGLYIFGFSGIFETI 120
QY 121 LITIDRYLAHVAVFALKARVTFEGVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
DB 121 LITIDRYLAHVAVFALKARVTFEGVTSVITWVAVFASLPGLIIFTRSQKGLHYTCSS 180
QY 181 HPPY 184
DB 181 HPPY 184

RESULT 13

PCT-US01-04153A-22
; Sequence 22, Application PC/TUS0104153A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115PCOD
; CURRENT APPLICATION NUMBER: PCT/US01/04153A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-04153A-22

Query Match 85.4%; Score 958; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.7e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYOVSSPIYDINVTSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60
DB 1 MDYOVSSPIYDINVTSEPCOKINVKQIARLLPLYSIVTFEGVGNMLVILLINCKR 60

QY	61	LLKSMIDYLLNLNATSDLEFFLLTPPMHAYAAAOBMGNNMCOLLTGLYFIQFSGTFFII	120
		LLKSMIDYLLNLNATSDLEFFLLTPPMHAYAAAOBMGNNMCOLLTGLYFIQFSGTFFII	120
Db	61	LKSMIDYLLNLNATSDLEFFLLTPPMHAYAAAOBMGNNMCOLLTGLYFIQFSGTFFII	120
QY	121	LLLTIDRYLAAYNAVAFALKARTVTPGVNVSVTITWVVAVFASLPGIIPTRSOKEGLHYTCSS	180
		LLLTIDRYLAAYNAVAFALKARTVTPGVNVSVTITWVVAVFASLPGIIPTRSOKEGLHYTCSS	180
Db	121	LLLTIDRYLAAYNAVAFALKARTVTPGVNVSVTITWVVAVFASLPGIIPTRSOKEGLHYTCSS	180
QY	181	HPFY 184	
Db	181	HPFY 184	

RESULT 14
PCT-US01-06699-1

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: Sequence 1, Application PC/TUS0106699
: GENERAL INFORMATION:
: APPLICANT: Progenics Pharmaceuticals, Inc., et al.
: TITLE OF INVENTION: SUFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
: FILE REFERENCE: 2004/61010-A-PC/TJPM/SHS/AX
: CURRENT APPLICATION NUMBER: PCT/US01/06699
: CURRENT FILING DATE: 2001-02-28
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 352
: TYPE: PPT
: ORGANISM: human
PCT-US01-06699-1

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Query Match: 85.4%; Score 958; DB 1; Length 352;
 Best Local Similarity: 100.0%; Pred. No. 6.7e-87;
 Matches 184; Conservative 0; Mismatches 0; Gaps 0;

RESULT 15
PCT-US01-10708-3
SEQUENCE 3 ANALYSIS OF AMINOACID SEQUENCE

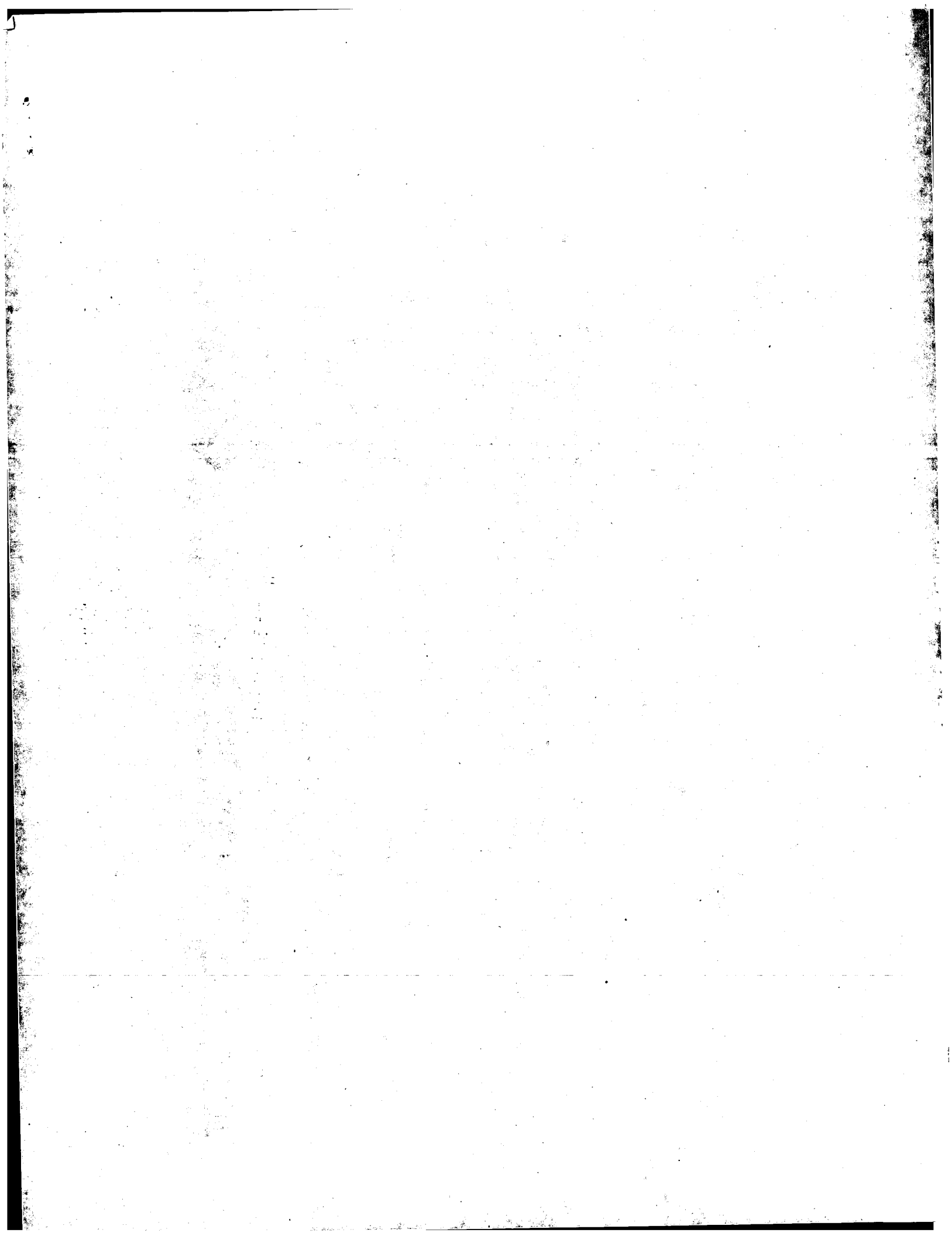
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: sequence 3. application PC/US01/0708
: GENERAL INFORMATION:
: APPLICANT: Genalabsance Pharmaceuticals Inc.
: APPLICANT: Choi, Julie
: APPLICANT: Killem, Stefania E.
: APPLICANT: Koshy, Beena
: TITLE OF INVENTION: Haplotypes of the CCR5 Gene
: FILE REFERENCE: MMH-0505CT CCR5
: CURRENT APPLICATION NUMBER: PCT/US01/10708
: CURRENT FILING DATE: 2001-04-04
: PRIOR APPLICATION NUMBER: 60/194,361
: PRIOR FILING DATE: 2000-04-05
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 352
: TYPE: PRT
: ORGANISM: Homo sapien
PCT-US01-10708-3

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Query Match	85.4%	Score 958	DB 1	Length 352
Best Local Similarity	100.0%	Pred. No. 6.7e-87		
Matches 184	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	1	MDYOVSPIYDINITYTSEPCOKINVKOIAARLLPPLYSLVIFGCFVGNMLVILLINCKR	60	
Db	1	MDYOVSPIYDINITYTSEPCOKINVKOIAARLLPPLYSLVIFGCFVGNMLVILLINCKR	60	
OY	61	LKSMDDIYLLNLAISDDLFFLLTVPPMAHYAAAMQMPGNTMOLLGLVPIGFSGIFPII	120	
Db	61	LKSMDDIYLLNLAISDDLFFLLTVPPMAHYAAAMQMPGNTMOLLGLVPIGFSGIFPII	120	
OY	121	LITIDRYLAAVVAEALKARTVTEGVTSVITWVAVAFASLPGIIFTRSOKEGLHYTCSS	180	
Db	121	LITIDRYLAAVVAEALKARTVTEGVTSVITWVAVAFASLPGIIFTRSOKEGLHYTCSS	180	
OY	181	HPFY 184		
Db	181	HPFY 184		

Search completed: June 3, 2003, 15:31:05
Job time : 171.635 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:19:46 ; Search time 47.7778 Seconds

(without alignments)
947.732 Million cell updates/sec

Title: US-09-939-226-6

Perfect score: 1132
Sequence: 1 MDYVSSPIYDINVTSEPC.....AACGHLLGNPNRSASVSK 215Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1005926 seqs, 210607049 residues

Total number of hits satisfying chosen parameters: 1005926

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_US02-29560-259
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	958	85.4	352	1 PCT-US02-29560-259	Sequence 259, App
2	958	85.4	352	1 PCT-US02-06345-1	Sequence 1, Appl
3	958	85.4	352	1 PCT-US03-03763-1	Sequence 1, Appl
4	958	85.4	352	5 US-09-949-002-303	Sequence 303, App
5	958	85.4	352	5 US-09-949-004-242	Sequence 242, App
6	958	85.4	352	6 US-10-086-814-1	Sequence 1, Appl
7	958	85.4	352	6 US-10-245-882-259	Sequence 259, App
8	958	85.4	352	6 US-10-323-214-1	Sequence 1, Appl
9	958	85.4	352	6 US-10-225-567A-352	Sequence 352, App
10	958	85.4	352	6 US-10-290-058A-6	Sequence 6, Appl
11	958	85.4	352	6 US-10-360-828-1	Sequence 1, Appl
12	958	85.4	352	6 US-10-239-423-67	Sequence 67, App
13	958	85.4	352	7 US-60-452-680-12568	Sequence 12568, A
14	958	85.4	352	7 US-60-453-135-7850	Sequence 7850, App
15	958	85.4	352	7 US-60-453-050-7850	Sequence 7850, App
16	958	85.4	352	7 US-60-455-444-4380	Sequence 4380, App
17	958	85.4	352	7 US-60-465-241-4380	Sequence 4380, App
18	958	85.4	352	7 US-60-466-412-7850	Sequence 7850, App
19	958	85.4	378	5 US-09-949-002-552	Sequence 552, App
20	958	85.4	378	5 US-09-949-004-442	Sequence 442, App
21	839	74.8	332	6 US-10-095-876A-2	Sequence 2, Appl
22	775	69.1	354	6 US-10-219-051B-10290	Sequence 10290, A
23	775	69.1	354	6 US-10-219-051B-10294	Sequence 10294, A
24	766	68.3	268	6 US-10-160-619-164	Sequence 164, App
25	762	67.9	268	6 US-10-160-619-162	Sequence 162, App
26	694	61.9	360	6 US-10-225-567A-460	Sequence 460, App

27	694	61.9	360	6 US-10-229-423-64	Sequence 64, Appl
28	694	61.9	360	7 US-60-452-680-12372	Sequence 12372, A
29	694	61.9	360	7 US-60-453-135-7700	Sequence 7700, App
30	694	61.9	360	7 US-60-453-050-7700	Sequence 7700, App
31	694	61.9	360	7 US-60-455-444-4289	Sequence 4289, App
32	694	61.9	360	7 US-60-465-241-4289	Sequence 4289, App
33	694	61.9	360	7 US-60-466-412-7700	Sequence 7700, App
34	694	61.9	374	5 US-09-949-004-244	Sequence 244, App
35	694	61.9	374	5 US-09-893-512A-13	Sequence 13, Appl
36	694	61.9	374	6 US-10-239-423-63	Sequence 63, Appl
37	694	61.9	374	6 US-10-219-051B-10292	Sequence 10292, A
38	694	61.9	374	7 US-60-452-680-12373	Sequence 12373, A
39	694	61.9	374	7 US-60-453-135-7701	Sequence 7701, App
40	694	61.9	374	7 US-60-455-444-4290	Sequence 4290, App
41	694	61.9	374	7 US-60-465-241-4290	Sequence 4290, App
42	694	61.9	374	7 US-60-466-412-7701	Sequence 7701, App
43	694	61.9	377	5 US-09-949-004-443	Sequence 443, App
44	694	61.9	377	5 US-09-949-004-443	Sequence 443, App
45	694	61.9	377	5 US-09-949-004-443	Sequence 443, App

ALIGNMENTS

RESULT 1
PCT-US02-29560-259
Sequence 259, Application PC/TUS0229560
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnik, Albert
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560
CURRENT FILING DATE: 2025-11-01
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 259
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-29560-259
Query Match 85.4%; Score 958; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. NO. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDYVSSPIYDINVTSEPCQKINVKQIAARLPLSLVIFGFGNMLYLILINCKR 60
DB 1 MDYVSSPIYDINVTSEPCQKINVKQIAARLPLSLVIFGFGNMLYLILINCKR 60
QY 61 LKSTDIYLLNLALSDFLLTVPFPAHYAAQNDGFTKCOLLTGLTFEFGGIFPII 120
DB 61 LKSTDIYLLNLALSDFLLTVPFPAHYAAQNDGFTKCOLLTGLTFEFGGIFPII 120
QY 121 LITDRIYLAHVHAFALKARTVTFGVYTSVITVAVFASLPGIIFRSGEGILHYCCS 180
DB 121 LITDRIYLAHVHAFALKARTVTFGVYTSVITVAVFASLPGIIFRSGEGILHYCCS 180
QY 181 HFPPY 184
DB 181 HFPPY 184
RESULT 2

PCT-US02-06345-1
; Sequence 1, Application PC/TUS0206345
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc., et al.
; TITLE OF INVENTION: Sulfated CCR5 Peptides For HIV-1 Infection
; FILE REFERENCE: 61010-AB1-PCR/JPM/JTL
; CURRENT APPLICATION NUMBER: PCT/US02/06345
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Human
PCT-US02-06345-1

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINTYSEPCQKINVKQIARLLPLYSLVTFEGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINTYSEPCQKINVKQIARLLPLYSLVTFEGVGNMLVILLINCKR 60
QY 61 LKSMDDIYLLNLAISDLFFLLVPPFAHAAAOQMPGNTMCOLLGLYIFGFSGIFETI 120
DB 61 LKSMDDIYLLNLAISDLFFLLVPPFAHAAAOQMPGNTMCOLLGLYIFGFSGIFETI 120
QY 121 LTTIDRYLAVHVAVALKARVTGVTSTVTVVAVFASLPGIIFTSQKGLHYTCSS 180
DB 121 LTTIDRYLAVHVAVALKARVTGVTSTVTVVAVFASLPGIIFTSQKGLHYTCSS 180
QY 181 HPPY 184
DB 181 HPPY 184

RESULT 3
PCT-US03-03763-1
; Sequence 1, Application PC/TUS0303763
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: METHODS FOR GENERATING ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-728
; CURRENT APPLICATION NUMBER: PCT/US03/03763
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-03763-1

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINTYSEPCQKINVKQIARLLPLYSLVTFEGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINTYSEPCQKINVKQIARLLPLYSLVTFEGVGNMLVILLINCKR 60
QY 61 LKSMDDIYLLNLAISDLFFLLVPPFAHAAAOQMPGNTMCOLLGLYIFGFSGIFETI 120
DB 61 LKSMDDIYLLNLAISDLFFLLVPPFAHAAAOQMPGNTMCOLLGLYIFGFSGIFETI 120

QY 121 LTTIDRYLAVHVAVALKARVTGVTSTVTVVAVFASLPGIIFTSQKGLHYTCSS 180
DB 121 LTTIDRYLAVHVAVALKARVTGVTSTVTVVAVFASLPGIIFTSQKGLHYTCSS 180
QY 181 HPPY 184
DB 181 HPPY 184

RESULT 4
US-09-949-002-303
; Sequence 303, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-303

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYVSSPIYDINTYSEPCQKINVKQIARLLPLYSLVTFEGVGNMLVILLINCKR 60
DB 1 MDYVSSPIYDINTYSEPCQKINVKQIARLLPLYSLVTFEGVGNMLVILLINCKR 60
QY 61 LKSMDDIYLLNLAISDLFFLLVPPFAHAAAOQMPGNTMCOLLGLYIFGFSGIFETI 120
DB 61 LKSMDDIYLLNLAISDLFFLLVPPFAHAAAOQMPGNTMCOLLGLYIFGFSGIFETI 120
QY 121 LTTIDRYLAVHVAVALKARVTGVTSTVTVVAVFASLPGIIFTSQKGLHYTCSS 180
DB 121 LTTIDRYLAVHVAVALKARVTGVTSTVTVVAVFASLPGIIFTSQKGLHYTCSS 180
QY 181 HPPY 184
DB 181 HPPY 184

RESULT 5
US-09-949-004-242
; Sequence 242, Application US/09949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000848
; CURRENT APPLICATION NUMBER: US/09/949,004
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 242
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Human
US-09-949-004-242

Query Match 85.4%; Score 958; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYVSSPIYDINTYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINTYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60

OY 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYFIFGFSGIFPII 120

OY 121 LTTIDRYLAHVAVFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LTTIDRYLAHVAVFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

OY 181 HFPY 184
DB 181 HFPY 184

RESULT 6

US-10-086-814-1
Sequence 1, Application US/10086814
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYVSSPIYDINTYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINTYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60

OY 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYFIFGFSGIFPII 120

OY 121 LTTIDRYLAHVAVFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LTTIDRYLAHVAVFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

OY 181 HFPY 184
DB 181 HFPY 184

RESULT 7

US-10-245-882-259
Sequence 259, Application US/10245882
GENERAL INFORMATION:
APPLICANT: Afari, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Glen, Kurt C.
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710US
CURRENT APPLICATION NUMBER: US/10/245,882
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/323,887
PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/325,114
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/340,944
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/355,145
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/355,257
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/369,899
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 259
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-245-882-259

Query Match 85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYVSSPIYDINTYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60
DB 1 MDYVSSPIYDINTYTSPCKINVKQIAARLLPPLYSLVIFGFGVGNMVLILLINCKR 60

OY 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYFIFGFSGIFPII 120
DB 61 LKSMTDIYLLNLAIISDLFFLLTPFMAHYAAQMDFGNTMCOQLTGLYFIFGFSGIFPII 120

OY 121 LTTIDRYLAHVAVFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180
DB 121 LTTIDRYLAHVAVFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSQEGLHYTCSS 180

OY 181 HFPY 184
DB 181 HFPY 184

RESULT 8

US-10-323-314-1
Sequence 1, Application US/10323314
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPM/MAF/DJR
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
US-10-323-314-1

Query Match 85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
DB      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
OY      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
DB      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
OY      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
DB      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
OY      181 HFPY 184
DB      181 HFPY 184

RESULT 9
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Birmer, Joseph P.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match      85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
DB      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
OY      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
DB      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
OY      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
DB      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
OY      181 HFPY 184
DB      181 HFPY 184

RESULT 10
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; GENERAL INFORMATION:
; APPLICANT: Sillas-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
; FILE REFERENCE: MP101-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match      85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
DB      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
OY      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
DB      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
OY      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
DB      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
OY      181 HFPY 184
DB      181 HFPY 184

RESULT 11
US-10-360-828-1
; Sequence 1, Application US/10360828
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-360-828-1

Query Match      85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
DB      1 MDYVSSPIYDINITYTSEPCOKINVKQIAARLLPPLYSLVFTFGFVGNMLVILLINCKR 60
OY      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
DB      61 LKSMTDIYLLNLAIISDLFFLLTPFPAHAYAAQMDFGNTMCOGLTGLYFIFGFSGIFETI 120
OY      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
DB      121 LTTIDRYLAVVAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSOKEGLHYTCSS 180
OY      181 HFPY 184
DB      181 HFPY 184

```

RESULT 12

US-10-239-423-67
Sequence 67, Application US/10239423
GENERAL INFORMATION:
APPLICANT: FORSSMANN, WOLF-GEORG; FORSSMANN, ULF; ADERMAN, KNUZ;
TITLE OF INVENTION: DIAGNOSTIC AGENT AND MEDICAMENT FOR EXAMINING THE
TITLE OF INVENTION: CELL SURFACE PROTEOME OF TUMOR AND INFLAMMATORY CELLS AND
TITLE OF INVENTION: FOR TREATING TUMOR DISEASES AND INFLAMMATORY DISEASES,
TITLE OF INVENTION: PREFERABLY WITH THE AID OF SPECIFIC CHEMOKINE
TITLE OF INVENTION: RECEPTOR ANALYSIS AND CHEMOKINE RECEPTOR/LIGAND INTERACTION
FILE REFERENCE: 022217US
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: DE10016013.1
PRIORITY FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 67
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67

Query Match 85.4%; Score 958; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVLILLINCKR 60
DB 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVLILLINCKR 60
OY 61 LKSTWDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFGGIFPII 120
DB 61 LKSTWDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFGGIFPII 120
OY 121 LTTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSOEGHLHYTCSS 180
DB 121 LTTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSOEGHLHYTCSS 180
OY 181 HFPY 184
DB 181 HFPY 184
RESULT 13
US-60-452-680-12568
Sequence 12568, Application US/60452680
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12568
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-60-452-680-12568

Query Match 85.4%; Score 958; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVLILLINCKR 60

DB 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVLILLINCKR 60
OY 61 LKSTWDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFGGIFPII 120
DB 61 LKSTWDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFGGIFPII 120
OY 121 LTTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSOEGHLHYTCSS 180
DB 121 LTTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSOEGHLHYTCSS 180
OY 181 HFPY 184
DB 181 HFPY 184

RESULT 14

US-60-453-135-7850
Sequence 7850, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7850
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-135-7850

Query Match 85.4%; Score 958; DB 7; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVLILLINCKR 60
DB 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVLILLINCKR 60
OY 61 LKSTWDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFGGIFPII 120
DB 61 LKSTWDIYLLNLAIISDLFFLLTVPFMAHYAAQMDFGNTMQLLTGLYIFGFGGIFPII 120
OY 121 LTTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSOEGHLHYTCSS 180
DB 121 LTTIDRYLAVVHAFALKARTVTEGVVTSVITWVAVFASLPGIIFTRSOEGHLHYTCSS 180
OY 181 HFPY 184
DB 181 HFPY 184

RESULT 15

US-60-453-050-7850
Sequence 7850, Application US/60453050
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7850
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens

OY 1 MDYOVSSPIYDINVTSEPCOKINVKQIAARLLPPLSLVIFGFGVGMVLILLINCKR 60

US-60-453-050-7850

Query Match 85.4%; Score 958; DB 7; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.2e-86;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 MDYQSSPYDINNYTSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLINCKR 60
DB	1 MDYQSSPYDINNYTSEPCOKINVKOIAARLLPPLYSLVIFGFGNMLVILLINCKR 60
QY	61 LKSMTDIYLLNLAIISDLFELLTPPMAHYAAQMDFGNTMCOLLTGLYFIFGFGSIFELI 120
DB	61 LKSMTDIYLLNLAIISDLFELLTPPMAHYAAQMDFGNTMCOLLTGLYFIFGFGSIFELI 120
QY	121 LFTIDRYLAVNAVPAKARTVFGVNTSVITWVAVAFASLPGILFTRSQKEGLHYTCSS 180
DB	121 LFTIDRYLAVNAVPAKARTVFGVNTSVITWVAVAFASLPGILFTRSQKEGLHYTCSS 180
QY	181 HFPY 184
DB	181 HFPY 184

Search completed: June 3, 2003, 15:33:14
 Job time : 47.7778 secs